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<110> MATSUDA, Akio et al.

<120> NF-kB ACTIVATING GENE

<130> 1254-0229P

<140> US 10/617,217
<141> 2003-07-11

<150> JP 2000-402288
<151> 2000-12-28

<150> JP 2001-088912
<151> 2001-03-26

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<150> US 60/258,315
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<170> PatentIn Ver. 2.0

<210> 1
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Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr
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Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser
        35   40   45

Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln
    50   55   60

Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly
65   70   75   80

Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly
                85   90   95

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Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr
            100             105             110

Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro
        115             120             125

Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser
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Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly
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Tyr Gly Gly Thr Arg Arg Arg
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<213> Homo sapiens

<220>
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gtctggaaag cagcacggct ttgcctcttt ctctgattat tattataagt ggtcctcggc  180

ggattcctgt aac atg agt gga ttg att acc atc gtg gta ctc ctt ggg     229
                Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly
                  1               5                      10

atc gcc ttt gta gtc tat aag ctg ttc ctg agt gac ggg cag tat tct     277
Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser
            15                  20                  25

cct cca ccg tac tct gag tat cct cca ttt tcc cac cgt tac cag aga     325
Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg
        30                  35                  40

ttc acc aac tca gca gga cct cct ccc cca ggc ttt aag tct gag ttc     373
Phe Thr Asn Ser Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe
 45                 50                  55                  60

aca gga cca cag aat act ggc cat ggt gca act tct ggt ttt ggc agt     421
Thr Gly Pro Gln Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser
                65                  70                  75

gct ttt aca gga caa caa gga tat gaa aat tca gga cca ggg ttc tgg     469
Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp
            80                  85                  90

aca ggc ttg gga act ggt gga ata cta gga tat ttg ttt ggc agc aat     517
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2

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Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn
        95              100             105


aga gcg gca aca ccc ttc tca gac tcg tgg tac tac ccg tcc tat cct    565
Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro
    110             115             120


ccc tcc tac cct ggc acg tgg aat agg gct tac tca ccc ctt cat gga    613
Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly
125             130             135             140


ggc tcg ggc agc tat tcg gta tgt tca aac tca gac acg aaa acc aga    661
Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg
            145             150             155


act gca tca gga tat ggt ggt acc agg aga cga taaagtagaa agttggagtc 714
Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg
            160             165


aaacactgga tgcagaaatt ttggattttt catcactttc tctttagaaa aaaagtacta  774

cctgttaaca attgggaaaa ggggatattc aaaagttcgg tggtgttatg tccagtgtag  834

cttttttgtat tctattattt gaggctaaaa gttgatgtgt dacaaaatac ttatgtgttg  894

tatgtcagtg taacatgcag atgtatattg cagtttttga aagtgatcat tactgtggaa  954

tgctaaaaat acattaattt ctaaaacctg tgatgcccta agaagcatta agaatgaagg 1014

tgttgtacta atagaaacta agtacagaaa atttcagttt taggtggttg tagctgatga 1074

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            20              25              30
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3

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Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His
        35              40                  45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
    50                  55                  60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
65                  70                  75                  80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
                85                  90                  95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
            100                 105                 110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
        115                 120                 125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
        130                 135                 140

Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
145                 150                 155                 160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
            165                 170                 175

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
        180                 185                 190

Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
        195                 200                 205

Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
    210                 215                 220

Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
225                 230                 235                 240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
            245                 250                 255

Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
            260                 265                 270

Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
        275                 280                 285

Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
    290                 295                 300

Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys
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Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr
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4

Arg Arg Arg

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<213> Homo sapiens

<220>
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<222> (115)..(1131)

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cccaggttcg gcccgtaggc gtctggcagc ccggcgccat cttcatcgag cgcc atg   117
                                                            Met
                                                            1

gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc   165
Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly
              5   10   15

ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac   213
Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp
          20   25   30

cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat   261
Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr
      35   40   45

gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa   309
Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys
  50   55   60   65

tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata   357
Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile
                  70   75   80

cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt   405
Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys
                  85   90   95

aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc   453
Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
              100   105   110

tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct   501
Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser
      115   120   125

tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa   549
Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys
130   135   140   145

5

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ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat    597
Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr
            150             155                 160

tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att    645
Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile
                165             170             175

acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc    693
Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe
            180             185             190

ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca    741
Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro
        195             200             205

ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc    789
Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
210                 215             220                 225

cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt    837
Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly
                230             235             240

gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa    885
Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu
            245             250             255

aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta    933
Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu
            260             265             270

gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg    981
Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser
        275             280             285

tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg   1029
Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg
290                 295             300                 305

gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca   1077
Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser
                310             315             320

aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg   1125
Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg
            325             330             335

aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggattttt   1181
Arg Arg

catcactttc tctttagaaa aaaagtacta cctgttaaca attgggaaaa ggggatattc  1241

aaaagttcgg tggtgttatg tccagtgtag ctttttgtat tctattattt gaggctaaaa  1301

gttgatgtgt gacaaaatac ttatgtgttg tatgtcagtg taacatgcag atgtatattg  1361
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6

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tgatgcccta agaagcatta agaatgaagg tgttgtacta atagaaacta agtacagaaa 1481

atttcagttt taggtggttg tagctgatga gttattacct catagagact gtaatattct 1541

atttggtatt atattatttg atgtttgctg ttcttcaaac atttaaatca agctttggac 1601

taattatgct aatttgtgag ttctgatcac ttttgagctc tgaagctttg aatcattcag 1661

tggtggagat ggccttctgg taactgaata ttaccttctg taggaaaagg tggaaaataa 1721

gcatctagaa ggttgttgtg aatgactctg tgctggcaaa aatgcttgaa acctctatat 1781

ttctttcgtt cataagaggt aaaggtcaaa tttttcaaca aaagtctttt aataacaaaa 1841

gcatgcagtt ctctgtgaaa tctcaaatat tgttgtaata gtctgtttca atcttaaaaa 1901

gaatcaataa aaacaaacaa ggg                                        1924
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<213> Homo sapiens

<400> 5

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            20                  25                  30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
            35                  40                  45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
        50                  55                  60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
 65                  70                  75                  80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
                85                  90                  95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
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Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser
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<212> DNA
<213> Homo sapiens

7

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236
                                                   Met Ala Gly Ala
                                                    1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
 5   10   15   20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
                25   30   35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
             40   45   50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
         55   60   65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
     70   75   80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
 85   90   95   100

atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg 572
Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu
                105   110   115

gac att gcc ttc aag cta aac aac caa atc agt taagtgtact ctcctctcat 625
Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser
                120   125

ccctttcttc cctttgagca ttgccctctt tgggttcttt ttgagccaat tctaataaaa 685

gtaaaaatgg taatagt   702

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<212> PRT
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8

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            20                  25                  30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
            35                  40                  45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
    50                  55                  60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65                  70                  75                  80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
            85                  90                  95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
            100                 105                 110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu
            115                 120                 125

Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala
    130                 135                 140

Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu
145                 150                 155                 160

Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr
            165                 170                 175

Tyr Glu Cys Asp Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly
            180                 185                 190

Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser
    195                 200                 205

Gly Lys Ser His Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr
    210                 215                 220

Pro Ser Gly Met Val Phe His Arg Val
225                 230
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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236
                                                Met Ala Gly Ala
                                                  1


att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att   284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
  5                  10                  15                  20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct   332
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
                25                  30                  35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat   380
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
                40                  45                  50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc   428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
                55                  60                  65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa   476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
           70                  75                  80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac   524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
 85                  90                  95                  100

atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg   572
Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu
               105                 110                 115

gac att gcc ttc aag cta aac aac caa atc aga gaa aat gca gaa gtc   620
Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val
               120                 125                 130

tcc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg   668
Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp
               135                 140                 145

act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc   716
Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe
   150                 155                 160

aca tct ccc aag act cca gag cat gag ggc cgt tac tat gaa tgt gat   764
Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp
165                 170                 175                 180

gtc ctt cct tac gcc cag cat ctt cat cat tat ggt gtg gta ttg gag   812
Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly Val Val Leu Glu
               185                 190                 195
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10

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gag gat cac cat gat gtc ccg acc ccc agt gct tct gga aaa agt cat    860
Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser Gly Lys Ser His
            200             205             210

ctt tgc cct tgg gat ttc cat gac ctt tat caa tat ccc agt gga atg    908
Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr Pro Ser Gly Met
        215             220             225

gtt ttc cat cgg gtt tgactggacc tggatgctgc tgtttggtga catccgacag    963
Val Phe His Arg Val
    230

ggcatcttct atgcgatgct tctgtccttc tggatcatct tctgtggcga gcacatgatg   1023

gatcagcacg agcggaacca catcgcaggg tattggaagc aagtcggacc cattgccgtt   1083

ggctccttct gcctcttcat atttgacatg tgtgagagag gggtacaact cacgaatccc   1143

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aatggcgatc tgggtgtcca tagtggggaa gaactccagc tcaccaccac tatcacccat   1623

gtggacggac ccactgagat ctacaagttg acccgcaagg aggcccagga gtaggaggct   1683

gcagcgcccg gctgggacgg tctctccata ccccagcccc tctaactaga gtggggagca   1743

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accagcggca tggacatttg tcagtttgcc ttctgacggt agcttttgga ggaagattcc   1863

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tcattgttaa ttagtgacat agtaacatct gtagcagctg gttagtaaac ctcatgtggg   1983

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gacatttttc ctgtttttaaa ttctaggata gattttaaca tcctttgcgg tcccagtcca   2103

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tatatcacca ggtagcccac tgagttaata tttaagttgt caatagataa gtgtccctgt   2223

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11

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<210> 9
<211> 198
<212> PRT
<213> Homo sapiens

<400> 9
Met Ala Thr Leu Trp Gly Gly Leu Leu Arg Leu Gly Ser Leu Leu Ser
 1   5   10   15

Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu Ser Asp
            20   25   30

Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro
            35   40   45

Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys
    50   55   60

Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro
 65   70   75   80

Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg
                85   90   95

Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu
                100   105   110

Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile
            115   120   125

Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp
    130   135   140

Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala
145   150   155   160

Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln
                165   170   175

Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp
            180   185   190

Arg His Val Val Leu Ser
            195

<210> 10
<211> 1498
<212> DNA
<213> Homo sapiens

12

<220>
<221> CDS
<222> (86)..(679)

<400> 10
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ctgtgggacc gctgggcccc cagcg atg gcg acc ctg tgg gga ggc ctt ctt   112
                                Met Ala Thr Leu Trp Gly Gly Leu Leu
                                 1   5

cgg ctt ggc tcc ttg ctc agc ctg tcg tgc ctg gcg ctt tcc gtg ctg   160
Arg Leu Gly Ser Leu Leu Ser Leu Ser Cys Leu Ala Leu Ser Val Leu
 10   15   20   25

ctg ctg gcg cag ctg tca gac gcc gcc aag aat ttc gag gat gtc aga   208
Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg
             30   35   40

tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat   256
Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr
                 45   50   55

aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag   304
Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu
             60   65   70

ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt   352
Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys
         75   80   85

gaa tgc aaa tat gaa gaa aga agc tct gtc aca atc aag gtt acc att   400
Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile
 90   95   100   105

ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg gta tat   448
Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val Tyr
                 110   115   120

ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca   496
Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala
             125   130   135

cag ttg ata cag agt gat gat gat att ggg gat cac cag cct ttt gca   544
Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro Phe Ala
         140   145   150

aat gca cac gat gtg cta gcc cgc tcc cgc agt cga gcc aac gtg ctg   592
Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn Val Leu
     155   160   165

aac aag gta gaa tat gca cag cag cgc tgg aag ctt caa gtc caa gag   640
Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu
170   175   180   185

cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc taattgggaa   689
Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser

13

```
Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser
              190                   195
```

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ttgaattcaa ggtgactaga aagaaacagg cagacaactg gaaagaactg actgggtttt  749

gctgggtttc attttaatac cttgttgatt tcaccaactg ttgctggaag attcaaaact  809

ggaagcaaaa acttgcttga ttttttttttc ttgttaacgt aataatagag acatttttaa  869

aagcacacag ctcaaagtca gccaataagt cttttcctat ttgtgacttt tactaataaa  929

aataaatctg cctgtaaatt atcttgaagt cctttacctg gaacaagcac tctcttttttc  989

accacatagt tttaacttga ctttcaagat aattttcagg gttttgttg ttgttgtttt  1049

ttgtttgttt gttttggtgg gagagggggag ggatgcctgg gaagtggtta acaacttttt  1109

tcaagtcact ttactaaaca aactttttgta aatagacctt accttctatt ttcgagtttc  1169

atttatattt tgcagtgtag ccagcctcat caaagagctg acttactcat ttgacttttg  1229

cactgactgt attatctggg tatctgctgt gtctgcactt catggtaaac gggatctaaa  1289

atgcctggtg gcttttcaca aaaagcagat tttcttcatg tactgtgatg tctgatgcaa  1349

tgcatcctag aacaaactgg ccatttgcta gtttactcta aagactaaac atagtcttgg  1409

tgtgtgtggt cttactcatc ttctagtacc tttaaggaca aatcctaagg acttggacac  1469

ttgcaataaa gaaattttat tttaaaccc                                    1498
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<210> 11
<211> 221
<212> PRT
<213> Homo sapiens
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<400> 11
Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly
 1               5                  10                  15

Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu
            20                  25                  30

Gln Ala Ala Gly Asp Ala Pro Pro Tyr Ser Ser Ile Ser Ala Glu
         35                  40                  45

Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro
     50                  55                  60

Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu
 65                  70                  75                  80

Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu
                 85                  90                  95

Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile
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14

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe
    115   120   125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala
    130   135   140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp
145   150   155   160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly
              165   170   175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe
              180   185   190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr
      195   200   205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr
    210   215   220

<210> 12
<211> 1864
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (153)..(815)

<400> 12
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cccctcggcc tcccagcgct cccaagccgc agcggccgcg ccccttcagc tagctcgctc 120

gctcgctctg cttccctgct gccggctgcg cc atg gcg ttg gcg ttg gcg gcg 173
                                      Met Ala Leu Ala Leu Ala Ala
                                       1   5

ctg gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag 221
Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln
          10   15   20

aat gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct 269
Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro
    25   30   35

cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac 317
Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr
40   45   50   55

aag gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca 365
Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr

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aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act   413
Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr
            75                  80                  85

atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat   461
Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp
        90                  95                  100

ttt gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg   509
Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met
    105                 110                 115

tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg   557
Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu
120                 125                 130                 135

tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca   605
Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser
                140                 145                 150

gga ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc   653
Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser
            155                 160                 165

acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg   701
Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val
        170                 175                 180

ttc ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat   749
Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr
    185                 190                 195

gca aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc   797
Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr
200                 205                 210                 215

aga gtt ctc ttt att tat taaagatgtt ttctggcaaa ggccttcctg          845
Arg Val Leu Phe Ile Tyr
                220

catttatgaa ttctctctca agaagcaaga gaacacctgc aggaagtgaa tcaagatgca  905

gaacacagag gaataatcac ctgctttaaa aaaataaagt actgttgaaa agatcatttc  965

tctctatttg ttcctaggtg taaaatttta atagttaatg cagaattctg taatcattga 1025

atcattagtg gttaatgttt gaaaaagctc ttgcaatcaa gtctgtgatg tattaataat 1085

gccttatata ttgtttgtag tcattttaag tagcatgagc catgtccctg tagtcggtag 1145

ggggcagtct tgctttattc atcctccatc tcaaaatgaa cttggaatta aatattgtaa 1205

gatatgtata atgctggcca tttttaaggg gttttctcaa aagttaaact tttgctatga 1265

ctgtgttttt gcacataatc catatttgct gttcaagtta atctagaaat ttattcaatt 1325
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16

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ctgtatgaac acctggaagc aaaatcatag tgcaaaaata catttaaggt gtggtcaaaa 1385

ataagtcttt aattggtaaa taataagcat taattttta tagcctgtat tcacaattct 1445

gcggtacctt attgtaccta agggattcta aaggtgttgt cactgtataa aacagaaagc 1505

actaggatac aaatgaagct taattactaa aatgtaattc ttgacactct ttctataatt 1565

agcgttcttc accccacccc ccaccccccac ccccttatt ttccttttgt ctcctggtga 1625

ttaggccaaa gtctgggagt aaggagagga ttaggtactt aggagcaaag aaagaagtag 1685

cttggaactt ttgagatgat ccctaacata ctgtactact tgcttttaca atgtgttagc 1745

agaaaccagt gggttataat gtagaatgat gtgctttctg cccaagtggt aattcatctt 1805

ggtttgctat gttaaaactg taaatacaac agaacattaa taaatatctc ttgtgtagc 1864
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<210> 13
<211> 242
<212> PRT
<213> Homo sapiens

<400> 13

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Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn
 1               5                  10                  15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser
            20                  25                  30

Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu
         35                  40                  45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val
      50                  55                  60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro
 65                  70                  75                  80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
               85                  90                  95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln
            100                 105                 110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
         115                 120                 125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
      130                 135                 140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
145                 150                 155                 160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
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17

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
         180   185   190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
         195   200   205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
         210   215   220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
225   230   235   240

Leu Leu

<210> 14
<211> 2324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (13)..(738)

<400> 14
gagccgggca gg atg gat cac cac cag ccg ggg act ggg cgc tac cag gtg   51
              Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val
                1   5   10

ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca   99
Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro
     15   20   25

cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca   147
Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala
 30   35   40   45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act   195
Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr
             50   55   60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat   243
Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr
             65   70   75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat   291
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp
             80   85   90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa   339
Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu
     95   100   105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc   387

18

```
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe
110             115             120         125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg   435
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu
                130             135             140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc   483
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser
            145             150             155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga   531
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly
        160             165             170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat   579
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp
    175             180             185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt   627
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe
190             195             200             205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta   675
Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu
            210             215             220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg   723
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg
            225             230             235

tat ttc ttc tta ttg tagagactgc atcaacccga cattcctttc ttataccaat   778
Tyr Phe Phe Leu Leu
        240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa   838

gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta   898

caagccattt ctgttcattc tttaagtatc tatatttcat ttgttttgca catatgcata   958

tgtgcccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag  1018

tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag  1078

tcttccagct tgtaaatgcc attgacttct gacctgacat ttagtataat aaaaatgaaa  1138

ttcttaacca tgtcaaatga tttagtttct ggctcttaga ctcatctggc agttctacac  1198

atgaaacatc ttttgttata tagggtgtat tgaaacctgc agtgctgatt attagaaagg  1258

atttgtcaga tttttgaaca tgatatttac attattattt aggaaaactc ttcctgtaaa  1318

taaccatgca taacttactt tctgcaatgt tttcttagaa attgtgtcca gatagctttc  1378

actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca  1438
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19

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cacacacata tatatattta gaaacgtgag tgttaaagat agaatttgtt ttaggacaaa 1498

ttttaagaaa atgtgggaat accaaatgtc ctttataaga aaaataaatt ttattttaag 1558

ggacatacta gttttaggga ttttcagatg ggaagctgca ttttttaggat tgcccatctt 1618

aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

tcaaagttaa ttttctaaat aagataattc tcatttgtgt ttgtctttta aaaggccaat 1738

aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918

gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038

tctgtttttc ctttcggtta tatctttggt tttgaatacc aacatttaaa atgatggtat 2098

tttatctttt aaacttaaaa attatttaat acagctatat ggaccttata aaattgattt 2158

cttatttatt attagacatt actactaaaa ggtacatcta actattcagg dacattttttc 2218

catttccaaa aaataaaatt tattatgctt tataacctct tctgtatttt ctaatttttt 2278

cattgtcttt gataaataaa acagtttgt tttgctaata tagcct            2324
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<210> 15
<211> 242
<212> PRT
<213> Homo sapiens

<400> 15
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Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn
 1               5                  10                  15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser
                20                  25                  30

Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu
            35                  40                  45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val
        50                  55                  60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro
 65                  70                  75                  80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
                85                  90                  95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln
            100                 105                 110
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20

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Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
         115              120              125
Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
    130              135              140
Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
145              150              155              160
Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
              165              170              175
Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
         180              185              190
Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
         195              200              205
Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
    210              215              220
Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
225              230              235              240
Leu Leu


<210> 16
<211> 2324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (13)..(738)

<400> 16
gagccgggca gg atg gat cac cac cag ccg ggg act ggg cgc tac cag gtg 51
           Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val
            1               5                  10

ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99
Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro
    15              20              25

cct act tca aac cca gca ccg cag att gtg cag gct gtg tct tca gca 147
Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala
 30              35              40              45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195
Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr
              50              55              60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243
Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr
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ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat    291
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp
        80              85                      90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa    339
Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu
        95              100                     105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc    387
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe
110                 115                 120                 125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg    435
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu
                130                 135                 140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc    483
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser
            145                 150                 155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga    531
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly
        160                 165                 170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat    579
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp
    175                 180                 185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt    627
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe
190                 195                 200                 205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta    675
Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu
                210                 215                 220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg    723
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg
                225                 230                 235

tat ttc ttc tta ttg tagagactgc atcaacccga cattcctttc ttataccaat   778
Tyr Phe Phe Leu Leu
        240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa  838

gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta  898

caagccattt ctgttcattc tttaagtatc tatatttcat ttgttttgca catatgcata  958

tgtgcccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag  1018

tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag  1078

tcttccagct tgtaaatgcc attgacttct gacctgacat ttagtataat aaaaatgaaa  1138
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22

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ttcttaacca tgtcaaatga tttagtttct ggctcttaga ctcatctggc agttctacac 1198

atgaaacatc ttttgttata tagggtgtat tgaaacctgc agtgctgatt attagaaagg 1258

atttgtcaga tttttgaaca tgatatttac attattattt aggaaaactc ttcctgtaaa 1318

taaccatgca taacttactt tctgcaatgt tttcttagaa attgtgtcca gatagctttc 1378

actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca 1438

cacacacata tatatattta gaaacgtgag tgttaaagat agaatttgtt ttaggacaaa 1498

ttttaagaaa atgtgggaat accaaatgtc ctttataaga aaaataaatt ttattttaag 1558

ggacatacta gttttaggga ttttcagatg ggaagctgca tttttaggat tgcccatctt 1618

aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

tcaaagttaa ttttctaaat aagataattc tcatttgtgt ttgtctttta aaaggccaat 1738

aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918

gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038

tctgtttttc ctttcggtta tatctttggt tttgaatacc aacatttaaa atgatggtat 2098

tttatctttt aaacttaaaa attatttaat acagctatat ggaccttata aaattgattt 2158

cttatttatt attagacatt actactaaaa ggtacatcta actattcagg gacatttttc 2218

catttccaaa aaataaaatt tattatgctt tataacctct tctgtatttt ctaatttttt 2278

cattgtcttt gataaataaa acagttttgt tttgctaata tagcct           2324
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<210> 17
<211> 336
<212> PRT
<213> Homo sapiens

<400> 17
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Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met
 1               5                  10                  15

Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr
            20                  25                  30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu
        35                  40                  45
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Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
    50              55              60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
65              70              75                      80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
                85              90              95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
            100             105             110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
        115             120             125

Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr
    130             135             140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
145             150             155             160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
            165             170             175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
            180             185             190

Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
    195             200             205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
    210             215             220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
225             230             235             240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
            245             250             255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
            260             265             270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
    275             280             285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
    290             295             300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
305             310             315             320

Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
            325             330             335
```

<210> 18
<211> 2636

24

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (53)..(1060)

<400> 18
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                                                           Met Ala
                                                            1

cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat   106
Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn
          5   10   15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg   154
Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala
         20   25   30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg   202
Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro
 35   40   45   50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg   250
Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala
                 55   60   65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac   298
Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
                 70   75   80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac   346
Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
             85   90   95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac   394
Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
    100   105   110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg   442
Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
115   120   125   130

cag att gtg cag gct gtg tct tca gca cca gca ctt gaa act gac tct   490
Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
                 135   140   145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca   538
Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
                 150   155   160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc   586
Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
             165   170   175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct   634

25

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Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
    180                 185                 190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag   682
Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
195                 200                 205                 210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga   730
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
                    215                 220                 225

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att   778
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile
                230                 235                 240

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata   826
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile
            245                 250                 255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa   874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys
    260                 265                 270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat   922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn
275                 280                 285                 290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt   970
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu
                295                 300                 305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa   1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu
                310                 315                 320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg           1060
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
    325                 330                 335

tagagactgc atcaacccga cattcctttc ttataccaat gtgaaatttc cagatcatct 1120

gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg ttttttgctta caagccattt ctgttcattc 1240

tttaagtatc tatatttcat ttgttttgca catatgcata tgtgcccatt taagatattt 1300

gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat 1360

cagtgtttga tataattgaa agagttgagt ggataaacag tcttccagct tgtaaatgcc 1420

attgacttct gacctgacat ttagtataat aaaaatgaaa ttcttaacca tgtcaaatga 1480

tttagtttct ggctcttaga ctcatctggc agttctacac atgaaacatc ttttgttata 1540

taaggtgtat tgaaacctgc agtgctgatt attagaaagg atttgtcaga tttttgaaca 1600
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26

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tgatatttac attattattt aggaaaactc ttcctgtaaa taaccatgca taacttactt 1660

tctgcaatgt tttcttagaa attgtgtcca gatagctttc actaattta aattaagtga 1720

actaaatata tatgtgtata tgtatacaca tatatataca cacacacata tatatattta 1780

gaaacgtgag tgttaaagat agaatttgtt ttaggacaaa ttttaagaaa atgtgggaat 1840

accaaatgtc ctttataaga aaaataaatt ttgtttttaag ggacatacca gttttaggga 1900

ttttcagatg ggaagctgca tttttaggat tgcccatctt aagagatctt gcaggaagag 1960

attgtattag atattatatt tatttcattt aagataattt caaagttaa ttttctaaat 2020

aagataattc tcatttgtgt ttgtcttta aaaggccaat aaaatatctt tcagtatcat 2080

tgtaataatt ttttagagtt taatttgtaa agcttagcaa ataaaatctt gtactatgaa 2140

tagcttcttg ctttatgact ttaggattaa cttgtaaaaa acatatcctg aactgagata 2200

tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg catatagga ctgtggggtc 2260

tgtgtgtgta gtgagagtgt gtagccacta ttataactgg aatttaattt acattcataa 2320

actactatat ttcccatctt gcaaatcatt ttatgtctca tctgttttttc ctttcggtta 2380

tatctttggt tttgaatacc aacatttaaa atgatggtat tttatcttttt aaacttaaaa 2440

attatttaat acagctatat ggaccttata aaattgattt cttatttatt attagacatt 2500

actactaaaa ggtacatcta actattcagg gacatttttc catttccaaa aaataaaatt 2560

tattatgctt tataacctct tctgtatttt ctaattttttt cattgtcttt gataaataaa 2620

acagttttgt tttgct                                                  2636


<210> 19
<211> 336
<212> PRT
<213> Homo sapiens

<400> 19
Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met
1               5                   10                  15

Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr
            20                  25                  30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu
        35                  40                  45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
    50                  55                  60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
65                  70                  75                  80
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27

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Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
                    85                  90                  95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
            100             105             110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
        115             120             125

Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr
    130             135             140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
145             150             155             160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
            165             170             175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
            180             185             190

Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
            195             200             205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
    210             215             220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
225             230             235             240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
            245             250             255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
            260             265             270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
            275             280             285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
    290             295             300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
305             310             315             320

Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
            325             330             335
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<210> 20
<211> 2636
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

28

<222> (53)...(1060)

<400> 20
cttacttttc catctcctcc cacccagcta taccctccca ctggcggcgc gg atg gca 58
                                                            Met Ala
                                                            1

cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat   106
Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn
            5   10   15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg   154
Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala
        20   25   30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg   202
Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro
35   40   45   50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg   250
Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala
                55   60   65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac   298
Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
                70   75   80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac   346
Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
            85   90   95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac   394
Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
        100   105   110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg   442
Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
115   120   125   130

cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct   490
Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
                135   140   145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca   538
Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
                150   155   160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc   586
Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
                165   170   175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct   634
Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
        180   185   190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag   682
Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu

29

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gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga    730
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
                215                 220                 225

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att    778
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile
                230                 235                 240

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata    826
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile
                245                 250                 255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa    874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys
        260                 265                 270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat    922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn
275                 280                 285                 290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt    970
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu
                295                 300                 305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa    1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu
                310                 315                 320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg              1060
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
        325                 330                 335

tagagactgc atcaacccga cattcctttc ttataccaat gtgaaatttc cagatcatct    1120

gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag    1180

acggagtttc gaaattgaat ggcagggtgg ttttgctta caagccattt ctgttcattc     1240

tttaagtatc tatatttcat ttgttttgca catatgcata tgtgcccatt aagatatttt    1300

gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat    1360

cagtgtttga tataattgaa agagttgagt ggataaacag tcttccagct tgtaaatgcc    1420

attgacttct gacctgacat ttagtataat aaaaatgaaa ttcttaacca tgtcaaatga    1480

tttagtttct ggctcttaga ctcatctggc agttctacac atgaaacatc ttttgttata    1540

taaggtgtat tgaaacctgc agtgctgatt attagaaagg atttgtcaga tttttgaaca    1600

tgatatttac attattattt aggaaaactc ttcctgtaaa taaccatgca taacttactt    1660

tctgcaatgt tttcttagaa attgtgtcca gatagctttc actaatttta aattaagtga    1720

actaaatata tatgtgtata tgtatacaca tatatataca cacacacata tatatattta    1780
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30

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gaaacgtgag tgttaaagat agaatttgtt ttaggacaaa ttttaagaaa atgtgggaat 1840

accaaatgtc ctttataaga aaaataaatt ttgtttaag ggacatacca gtttaggga 1900

ttttcagatg ggaagctgca ttttaggat tgcccatctt aagagatctt gcaggaagag 1960

attgtattag atattatatt tatttcattt aagataattt tcaaagttaa ttttctaaat 2020

aagataattc tcatttgtgt ttgtctttta aaaggccaat aaaatatctt tcagtatcat 2080

tgtaataatt ttttagagtt taatttgtaa agcttagcaa ataaaatctt gtactatgaa 2140

tagcttcttg ctttatgact ttaggattaa cttgtaaaaa acatatcctg aactgagata 2200

tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg gcatatagga ctgtggggtc 2260

tgtgtgtgta gtgagagtgt gtagccacta ttataactgg aatttaattt acattcataa 2320

actactatat ttcccatctt gcaaatcatt ttatgtctca tctgttttc ctttcggtta 2380

tatctttggt tttgaatacc aacatttaaa atgatggtat tttatctttt aaacttaaaa 2440

attatttaat acagctatat ggaccttata aaattgattt cttatttatt attagacatt 2500

actactaaaa ggtacatcta actattcagg gacattttc catttccaaa aaataaaatt 2560

tattatgctt tataacctct tctgtatttt ctaatttttt cattgtcttt gataaataaa 2620

acagttttgt tttgct                                                 2636


<210> 21
<211> 76
<212> PRT
<213> Homo sapiens

<400> 21
Met Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr
  1               5                  10                  15

Lys Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val
                20                  25                  30

Ser Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn
            35                  40                  45

Lys Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr
        50                  55                  60

Lys Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp
 65                  70                  75


<210> 22
<211> 1085
<212> DNA
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31

<213> Homo sapiens

<220>
<221> CDS
<222> (176)..(403)

<400> 22
gggctagcgg cctgggttgg gctttgtagc tgctccgcag gcccagcccg ggccgcgctc 60

gcagagtcct aggcggtgcg cggcctcctg cctcctccct cctcggcggt cgcggcccgc 120

cggcctccgc ggtgcctgcc ttcgctctca ggttgaggag ctcaagcttg ggaaa atg 178
                                                                Met
                                                                1

gtg tgc att cct tgt atc gtc att cca gtt ctg ctc tgg atc tac aaa 226
Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys
              5   10   15

aaa ttc ctg gag cca tat ata tac cct ctg gtt tcc ccc ttc gtt agt 274
Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser
          20   25   30

cgt ata tgg cct aag aaa gca ata caa gaa tcc aat gat aca aac aaa 322
Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys
          35   40   45

ggc aaa gta aac ttt aag ggt gca gac atg aat gga tta cca aca aaa 370
Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys
 50   55   60   65

gga cca aca gaa atc tgt gat aaa aag aaa gac taaagaaatt ttcctaaagg 423
Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp
                  70   75

accccatcat ttaaaaaatg gacctgataa tatgaagcat cttccttgta attgtctctg 483

acctttttat ctgagaccgg aattcaggat aggagtctag atatttacct gatactaatc 543

aggaaatata tgatatccgt atttaaaatg tagttagtta tatttaatga cctcattcct 603

aagttccttt ttcgttaatg tagctttcat ttctgttatt gctgtttgaa taatatgatt 663

aaatagaagg tttgtgccag tagacattat gttactaaat cagcacttta aaatctttgg 723

ttctctaatt catatgaatt tgctgtttgc tctaatttct ttgggctctt ctaatttgag 783

tggagtacaa ttttgttgtg aaacagtcca gtgaaactgt gcagggaaat gaaggtagaa 843

ttttgggagg taataatgat gtgaaacata aagatttaat aattactgtc caacacagtg 903

gagcagcttg tccacaaata tagtaattac tatttattgc tctaaggaag attaaaaaaa 963

gatagggaaa aggggggaaac ttctttgaaa aatgaaacat ctgttacatt aatgtctaat 1023

tataaaattt taatccttac tgcatttctt ctgttcctac aaatgtatta acattcagt 1083

32

<210> 23
<211> 84
<212> PRT
<213> Homo sapiens

<400> 23
Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu
 1   5   10   15

Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
            20   25   30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
         35   40   45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp
     50   55   60

Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser
 65   70   75   80

Leu Ser Gly Leu

<210> 24
<211> 1593
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (65)..(316)

<400> 24
agcgtcgcct cacgcggagc agagctgagc tgaagcggga cccggagccc gagcagccgc 60

cgcc atg gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc 109
     Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile
      1   5   10   15

ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa 157
Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys
            20   25   30

gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag 205
Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln
         35   40   45

att ccc ctg ttt ggg atc atg tct tca gat tca gct gac cct ttc tat 253
Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr
     50   55   60

tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac 301

33

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  Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His
       65                  70                  75


tct ctc tct ggc ctt tagggagtcc cctcttagga caggcactgc ccagcagcaa   356
Ser Leu Ser Gly Leu
 80


gggcagcaga gttgggtgct aagatcctga ggagctcgag gtttcgagct ggctttagac   416

attggtggga ccaaggatgt tttgcaggat gccctgatcc taagaagggg gcctgggggt   476

gcgtgcagcc tgtcggggag accccactct gtgcacctat tggctcttct agctgactct   536

tctcgttggg cttagagtct gcctgtttct gctagctccg tgtttagtcc acttgggtca   596

tcagctctgc caagctgagc ctggccaagc taggtggaca gacccttgca gtgatgtccg   656

tttgtccaga ttctgccagt catcactgga cacgtctcct cgcagctgcc ctagcaaggg   716

gagacattgt ggtagctatc agacatggac agaaactgac ttagtgctca caagccccta   776

caccttctgg gctgaagatc acccagctgt gttcagaatt ttcttactgt gcttaggact   836

gcacgcaagt gagcagacac caccgacttc ctttctgcgt caccagtgtc gtcagcagag   896

agaggacagc acaggctcaa ggttggtagt gaagtcaggt tcggggtgca tgggctgtgg   956

tggtggtgat cagttgctcc agtgtttgaa ataagaagac tcatgtttat gtctggaata   1016

agttctgttt gtgctgacag gtgaccttgc tggcagtgct agccaggaaa cagagtgacc   1076

aagggacaag aagggacttg cctaaagcca cccagcaact cagcagcaga accaagatgg   1136

gccccaggct cctccatatg gcccagggct taccaccctа tcacacgtgg ccttgtctag   1196

acccagtcct gagcagggga gaggctcttg agacctgatg ccctcctacc cacatggttc   1256

tcccactgcc ctgtctgctc tgctgctaca gaggggcagg gcctccccca gcccacgctt   1316

aggaatgctt ggcctctggc aggcaggcag ctgtacccaa gctggtgggc aggggggctgg   1376

aaggcaccag gcctcaggag gagcccccata gtcccgcctg cagcctgtaa ccatcggctg   1436

ggccctgcaa ggcccacact cacgccctgt gggtgatggt cacggtgggt gggtggggggc   1496

tgaccccagc ttccagggga ctgtcactgt ggacgccaaa atggcataac tgagataagg   1556

tgaataagtg acaaataaag ccagtttttt acaaggt                           1593



<210> 25
<211> 179
<212> PRT
<213> Homo sapiens

<400> 25
Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu


                                 34
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Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
          20              25              30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
          35              40              45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala
      50              55              60

Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys
 65              70              75              80

Thr Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln
              85              90              95

Leu Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met
          100             105             110

Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly
          115             120             125

Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile
      130             135             140

Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr
145             150             155             160

Phe Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala
              165             170             175

Leu Leu Phe
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<210> 26
<211> 1820
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (114)..(650)

<400> 26
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acgcggagca gagctgagct gaagcgggac ccggagcccg agcagccgcc gcc atg      116
                                                            Met
                                                            1

gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc ctg ccg  164
Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro
              5              10              15

gaa att cag aag cca gag agg aag att cag ttt aag gag aaa gtg ctg  212
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```
        Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu
              20                  25                  30

tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag att ccc    260
Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro
     35                  40                  45

ctg ttt ggg atc atg tct tca gat tca gct gac ccg gtc cat gca gtt    308
Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala Val
 50                  55                  60                  65

gta tac ata gtg ttc atg ctg ggc tcc tgt gca ttc ttc tcc aaa acg    356
Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr
                 70                  75                  80

tgg att gag gtc tca ggt tcc tct gcc aaa gat gtt gca aag cag ctg    404
Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln Leu
                 85                  90                  95

aag gag cag cag atg gtg atg aga ggc cac cga gag acc tcc atg gtc    452
Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met Val
             100                 105                 110

cat gaa ctc aac cgg tac atc ccc aca gcc gcg gcc ttt ggt ggg ctg    500
His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu
     115                 120                 125

tgc atc ggg gcc ctc tcg gtc ctg gct gac ttc cta ggc gcc att ggg    548
Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile Gly
130                 135                 140                 145

tct gga acc ggg atc ctg ctc gca gtc aca atc atc tac cag tac ttt    596
Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe
                 150                 155                 160

gag atc ttc gtt aag gag caa agc gag gtt ggc agc atg ggg gcc ctg    644
Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala Leu
             165                 170                 175

ctc ttc tgagcccgtc tcccggacag gttgaggaag ctgctccaga agcgcctcgg    700
Leu Phe

aaggggagct ctcatcatgg cgcgtgctgc tgcggcatat ggacttttaa taatgttttt 760

gaatttcgta ttctttcatt ccactgtgta aagtgctaga cattttccaa tttaaaattt 820

tgctttttat cctggcactg gcaaaagaa ctgtgaaagt gaatttattc agccgactgc 880

cagagaagtg ggaatggtat aggattgtcc ccaagtgtcc atgtaacttt tgttttaacc 940

tttgcacctt ctcagtgctg tatgcggctg cagccgtctc acctgtttcc ccacaaaggg 1000

aatttctcac tctggttgga agcacaaaca ctgaaatgtc tacgtttcat tttggcagta 1060

gggtgtgaag ctgggagcag atcatgtatt tcccggagac atgggacctt gctggcatgt 1120

ctccttcaca atcaggcgtg ggaatatctg gcttaggact gtttctctct aagacaccat 1180
```

36

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tgttttccct tattttaaaa gtgatttttt taaggacaga acttcttcca aaagagaggg 1240

atggctttcc cagaagacac tctggagacc ttgctggcag tgctagccag gaaacagagt 1300

gaccaaggga caagaaggga cttgcctaaa gccacccagc aactcagcag cagaaccaag 1360

atgggcccca ggctcctcca tatggcccag ggcttaccac cctatcacac gtggccttgt 1420

ctagacccag tcctgagcag gggagaggct cttgagacct gatgccctcc tacccacatg 1480

gttctcccac tgccctgtct gctctgctgc tacaragggg cagggcctcc cccagcccac 1540

gcttaggaat gcttggcctc tggcaggcag gcagctgtac ccaagctggt gggcaggggg 1600

ctggaaggca ccaggcctca ggaggagccc catagtcccg cctgcagcct gtaaccatcg 1660

gctgggccct gcaaggccca cactcacgcc ctgtgggtga tggtcacggt gggtgggtgg 1720

gggctgaccc cagcttccag gggactgtca ctgtggacgc caaaatggca taactsasat 1780

aaggtgaata agtgacaaat aaagccagtt ttttacaagg                         1820
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<400> 27
Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
 1               5                  10                  15

Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
            20                  25                  30

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
        35                  40                  45

Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
    50                  55                  60

Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
65                  70                  75                  80

Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
            85                  90                  95

Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
            100                 105                 110

Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
        115                 120                 125

Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
    130                 135                 140
```

37

```
-His Ser Val Leu Pro -Trp Ser Trp Trp Trp Gly Val Lys Ile-Ala Pro
145             150             155             160

Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
                165             170             175

Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln
            180             185             190

Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
            195             200             205

Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
    210             215             220

Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
225             230             235             240

Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
                245             250             255

Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
            260             265             270

Ile Ala Lys Val Lys Ala Asn
            275
```

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<210> 28
<211> 1472
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (119)..(955)

<400> 28
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tgctccctcc gagcgctccg ccgttgcccg cctggcccct acggagtcct tagccagg    118

atg gag gct gtt gtg aac ttg tac caa gag gtg atg aag cac gca gat  166
Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
 1               5               10              15

ccc cgg atc cag ggc tac cct ctg atg ggg tcc ccc ttg cta atg acc  214
Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
            20              25              30

tcc att ctc ctg acc tac gtg tac ttc gtt ctc tca ctt ggg cct cgc  262
Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
        35              40              45

atc atg gct aat cgg aag ccc ttc cag ctc cgt ggc ttc atg att gtc  310
Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
    50              55              60
```

```
tac aac ttc tca ctg gtg gca ctc tcc ctc tac att gtc tat gag ttc    358
Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
 65                  70              75                  80

ctg atg tcg ggc tgg ctg agc acc tat acc tgg cgc tgt gac cct gtg    406
Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
                 85                  90                  95

gac tat tcc aac agc cct gag gca ctt agg atg gtt cgg gtg gcc tgg    454
Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
                100             105                 110

ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt    502
Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
        115                 120                 125

att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat    550
Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
        130                 135                 140

cac tct gtg ctt ccc tgg agc tgg tgg tgg ggg gta aag att gcc ccg    598
His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro
145                 150                 155                 160

gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc    646
Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
                165                 170                 175

ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa    694
Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln
                180                 185                 190

ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag    742
Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
        195                 200                 205

ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc    790
Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
        210                 215                 220

tgt aac tac cag tac cca gtc att att cac ctc atc tgg atg tat ggc    838
Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
225                 230                 235                 240

acc atc ttc ttc atg ctg ttc tcc aac ttc tgg tat cac tct tat acc    886
Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
                245                 250                 255

aag ggc aag cgg ctg ccc cgt gca ctt cag caa aat gga gct cca ggt    934
Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
                260                 265                 270

att gcc aag gtc aag gcc aac tgagaagcat ggcctagata ggcgcccacc      985
Ile Ala Lys Val Lys Ala Asn
                275
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39

taagtgcctc aggactgcac cttagggcag tgtccgtcag tgccctctcc acctacacct 1045

gtgaccaagg cttatgtggt caggactgag cagggactg gccctcccct ccccacagct 1105

gctctacagg gaccacggct ttggttcctc acccacttcc cccgggcagc tccagggatg 1165

tggcctcatt gctgtctgcc actccagagc tggggctaa aagggctgta cagttatttc 1225

cccctccctg ccttaaaact tgggagagga gcactcaggg ctggccccac aaagggtctc 1285

gtggcctttt tcctcacaca gaagaggtca gcaataatgt cactgtggac ccagtctcac 1345

tcctccaccc cacacactga agcagtagct tctgggccaa aggtcagggt gggcggggc 1405

ctgggaatac agcctgtgga ggctgcttac tcaacttgtg tcttaattaa aagtgacaga 1465

ggaaacc   1472

<210> 29
<211> 137
<212> PRT
<213> Homo sapiens

<400> 29
Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu
 1   5   10   15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu
               20   25   30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser
           35   40   45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
       50   55   60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
65   70   75   80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
               85   90   95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
           100   105   110

Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala
           115   120   125

Tyr Met Asp Ala Pro Lys Ala Ala Leu
   130   135

<210> 30
<211> 1788
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (145)..(555)

<400> 30
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ggaaattgaa actgagtggc ccacgatggg aagagggggaa agcccagggg tacaggaggc 120

ctctgggtga aggcagaggc taac atg ggg ttc gga gcg acc ttg gcc gtt   171
                                Met Gly Phe Gly Ala Thr Leu Ala Val
                                 1   5

ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc ttc   219
Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe
 10   15   20   25

acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg   267
Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro
                30   35   40

gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct   315
Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro
                45   50   55

cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc   363
Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly
            60   65   70

tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac cca   411
Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro
     75   80   85

atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg gcc   459
Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala
 90   95   100   105

tac cac gag acc ctg gct gga gga gca gcc gcg ccc tac ccc gcc agc   507
Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser
                110   115   120

cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctc   555
Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu
                125   130   135

tgagcattcc ctggcctctc tggctgccac ttggttatgt tgtgtgtgtg cgtgagtggt 615

gtgcaggcgc ggttccttac gccccatgtg tgctgtgtgt gtccaggcac ggttccttac 675

gccccatgtg tgctgtgtgt gtcctgcctg tatatgtggc ttcctctgat gctgacaagg 735

tggggaacaa tccttgccag agtgggctgg gaccagactt tgttctcttc ctcacctgaa 795

attatgcttc ctaaaatctc aagccaaact caaagaatgg ggtggtgggg ggcaccctgt 855

gaggtggccc ctgagaggtg ggggcctctc cagggcacat ctggagttct tctccagctt 915

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acccctagggt gaccaagtag ggcctgtcac accagggtgg cgcagctttc tgtgtgatgc 975

agatgtgtcc tggtttcggc agcgtagcca gctgctgctt gaggccatgg ctcgtccccg 1035

gagttggggg tacccgttgc agagccaggg acatgatgca ggcgaagctt gggatctggc 1095

caagttggac tttgatcctt tgggcagatg tcccattgct ccctggagcc tgtcatgcct 1155

gttggggatc aggcagcctc ctgatgccag aacacctcag gcagagccct actcagctgt 1215

acctgtctgc ctggactgtc ccctgtcccc gcatctcccc tgggaccagc tggagggcca 1275

catgcacaca cagcctagct gcccccaggg agctctgctg cccttgctgg ccctgccctt 1335

cccacaggtg agcagggctc ctgtccacca gcacactcag ttctcttccc tgcagtgttt 1395

tcattttatt ttagccaaac attttgcctg ttttctgttt caaacatkat agttgatatg 1455

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tgagtccctg cttcccgaca ccagcctcat ggaatatgca caactcctg tacccccagtc 1575

cacggtgttc tggcagcagg gacacctggg ccaatgggcc atctggacca aaggtggggt 1635

gtggggccct ggatggcagc tctggcccag acatgaatac ctcgtgttcc tcctccctct 1695

attactgttt caccagagct gtcttagctc aaatctgttg tgtttctgag tctagggtct 1755

gtacacttgt ttataataaa tgcaatcgtt tgg                                1788


<210> 31
<211> 118
<212> PRT
<213> Homo sapiens

<400> 31
Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu
 1               5                  10                  15


Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu
                20                  25                  30


Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser
            35                  40                  45


Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Ser Val Pro Pro
        50                  55                  60


Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
 65                  70                  75                  80


Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
                85                  90                  95


Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
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Glu Cys Pro Cys Gln Leu
        115

<210> 32
<211> 1908
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (91)..(444)

<400> 32
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ggaggcctct gggtgaaggc agaggctaac atg ggg ttc gga gcg acc ttg gcc 114
                                  Met Gly Phe Gly Ala Thr Leu Ala
                                   1   5

gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc 162
Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys
    10   15   20

ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt 210
Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg
 25   30   35   40

ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat 258
Pro Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr
            45   50   55

cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag 306
Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln
            60   65   70

ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac 354
Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr
        75   80   85

cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg 402
Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro
    90   95   100

gcc tac cac gag acc ctg gct ggt gag tgc ccc tgc caa ctc 444
Ala Tyr His Glu Thr Leu Ala Gly Glu Cys Pro Cys Gln Leu
105   110   115

tagccctgcc cgacttcccg agtctctgcc agcatccctc gggcacccat cccaaactac 504

atcactcaac aggcctctgc ccctttctgc ttgcctgcca ctcacacggc agcccaccat 564

gctcacagcc aaccagggtc ctctctgctt tcaggaggag cagccgcgcc ctaccccgcc 624

agccagcctc cttacaaccc ggcctacatg gatgccccga aggcggccct ctgagcattc 684

43

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cctggcctct ctggctgcca cttggttatg ttgtgtgtgt gcgtgagtgg tgtgcaggcg 744

cggttcctta cgccccatgt gtgctgtgtg tgtccaggca cggttcctta cgccccatgt 804

gtgctgtgtg tgtcctgcct gtatatgtgg cttcctctga tgctgacaag gtggggaaca 864

atccttgcca gagtgggctg ggaccagact ttgttctctt cctcacctga aattatgctt 924

cctaaaatct caagccaaac tcaaagaatg gggtggtggg gggcaccctg tgaggtggcc 984

cctgagaggt gggggcctct ccagggcaca tctggagttc ttctccagct taccctaggg 1044

tgaccaagta gggcctgtca caccagggtg gcgcagcttt ctgtgtgatg cagatgtgtc 1104

ctggtttcgg cagcgtagcc agctgctgct tgaggccatg gctcgtcccc ggagttgggg 1164

gtacccgttg cagagccagg gacatgatgc aggcgaagct tgggatctgg ccaagttgga 1224

ctttgatcct ttgggcagat gtcccattgc tccctggagc ctgtcatgcc tgttggggat 1284

caggcagcct cctgatgcca gaacacctca ggcagagccc tactcagctg tacctgtctg 1344

cctggactgt cccctgtccc cgcatctccc ctgggaccag ctggagggcc acatgcacac 1404

acagcctagc tgcccccagg gagctctgct gcccttgctg ccctgccct tcccacaggt 1464

gagcagggct cctgtccacc agcacactca gttctcttcc ctgcagtgtt ttcattttat 1524

tttagccaaa cattttgcct gttttctgtt tcaaacatga tagttgatat gagactgaaa 1584

cccctggggtt gtggagggaa attggctcag agatggacaa cctggcaact gtgagtccct 1644

gcttcccgac accagcctca tggaatatgc aacaactcct gtaccccagt ccacggtgtt 1704

ctggcagcag ggacacctgg gccaatgggc catctggacc aaaggtgggg tgtggggccc 1764

tggatggcag ctctggccca gacatgaata cctcgtgttc ctcctccctc tattactgtt 1824

tcaccagagc tgtcttagct caaatctgtt gtgtttctga gtctagggtc tgtacacttg 1884

tttataataa atgcaatcgt ttgg                                          1908


<210> 33
<211> 168
<212> PRT
<213> Homo sapiens

<400> 33
Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro Val Gln
 1               5                  10                  15

Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro Gln Ala
            20                  25                  30

Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr Arg Pro
```

44

```
Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser Ala Ala
    50                  55                  60

Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val Ala Val
65                  70                  75                  80

Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val Gly Pro
                85                  90                  95

Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr Asp Ala
            100                 105                 110

Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro Pro Pro
            115                 120                 125

Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met Gln Gly
    130                 135                 140

Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met Gly Gly
145                 150                 155                 160

Ser Asp Gly Gly Tyr Thr Ile Trp
                165
```

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<210> 34
<211> 1897
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (70)..(573)

<400> 34
ctccgaacag gaagaggacg aaaaaaataa ccgtccgcga cgccgagaca aaccggaccc 60

gcaaccacc atg aac agc aaa ggt caa tat cca aca cag cca acc tac cct 111
          Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro
          1               5                   10

gtg cag cct cct ggg aat cca gta tac cct cag acc ttg cat ctt cct 159
Val Gln Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro
15                  20                  25                  30

cag gct cca ccc tat acc gat gct cca cct gcc tac tca gag ctc tat 207
Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr
                35                  40                  45

cgt ccg agc ttt gtg cac cca ggg gct gcc aca gtc ccc acc atg tca 255
Arg Pro Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser
            50                  55                  60

gcc gca ttt cct gga gcc tct ctg tat ctt ccc atg gcc cag tct gtg 303
Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val
```

45

```
gct gtt ggg cct tta ggt tcc aca atc ccc atg gct tat tat cca gtc   351
Ala Val Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val
        80              85              90

ggt ccc atc tat cca cct ggc tcc aca gtg ctg gtg gaa gga ggg tat   399
Gly Pro Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr
 95              100             105             110

gat gca ggt gcc aga ttt gga gct ggg gct act gct ggc aac att cct   447
Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro
                115             120             125

cct cca cct cct gga tgc cct ccc aat gct gct cag ctt gca gtc atg   495
Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met
            130             135             140

cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg   543
Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met
        145             150             155

ggt ggt tca gat ggt ggc tac acc atc tgg tgaggaacca aggccacctc     593
Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp
 160             165

tgtgccggga aagacatcac ataccttcag cacttctcac aatgtaactg ctttagtcat   653

attaacctga agttgcagtt tagacacatg ttgttggggt gtctttctgg tgcccaaact   713

ttcaggcact tttcaaattt aataaggaac catgtaatgg tagcagtacc tccctaaagc   773

attttgaggt aggggaggta tccattcata aaatgaatgt gggtgaagcc gccctaagga   833

ttttccttta atttctctgg agtaatactg taccatactg tctttgctt ttagtaataa    893

aacatcaaat taggtttgga gggaactttg atcttcctaa gaattaaagt tgccaaatta   953

ttctgattgg tctttaatct cctttaagtc tttgatatat attacttgtt ataaatggaa   1013

cgcattagtt gtctgccttt tcctttccat cccttgcccc acccatccca tctccaaccc   1073

tagtcttcca tttcctcccg ccagtctcca ttgaatcaat ggtgcaggac agaaagccag   1133

tcagactaat ttccttcttt cctcgcactt ctccccactc gtcatctttt aactagtgtt   1193

tcacaaggat cctctgaaac cctctctgtg ccccaagtac agatgccatt acttctgctt   1253

tcgtatctcc tcaggcaaaa gtggagggtg ccttatgggc cctcctcata ggttgtctct   1313

gcatacacga acctaaccca aatttgcttt ggtgccagaa aaactgagct atgtttgaac   1373

aaagatgtcg tgcaaactgt actgtgaaca acagttggtt taaaatatga ggggcaagga   1433

ggaggatgca tttcaaaagc ttgattgatg tgttcagagc taaattaaga ggagttttca   1493

gatcaaaaac tggttaccat tttttgtcag agtgtctgat gcggccactc attcggctcc   1553
```

46

```
ccagaattcc tagactgggt taatagggtc atattgtgaa tgtctcacta caaaatgact 1613

tgagtccagt gaaatctcat tagggtttaa gaatatttca gggatcctta atgttttgat 1673

ttttgttttc tgaaattgga ttttatttta ttttatctta taatttcagt tcatctaaat 1733

tgtgtgttct gtacatgtga tgtttgactg taccattgac tgttatggaa gttcagcgtt 1793

gtatgtctct ctctacactg tggtgcactt aacttgtgga atttttatac taaaaatgta 1853

gaataaagac tattttgaag atttgaataa agtgatgaag ttgc                 1897
```

<210> 35
<211> 455
<212> PRT
<213> Homo sapiens

<400> 35

```
Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu
 1               5                  10                  15

Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp
            20                  25                  30

Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe
            35                  40                  45

Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly
    50                  55                  60

Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys
65                  70                  75                  80

Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr
                85                  90                  95

Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe
            100                 105                 110

Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly
            115                 120                 125

Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu
    130                 135                 140

Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu
145                 150                 155                 160

Leu Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr
                165                 170                 175

Phe Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg
            180                 185                 190

Leu Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala
```

47

Met Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro
210   215   220

Ser Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly
225   230   235   240

Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu
          245   250   255

Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys
          260   265   270

Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe
          275   280   285

Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala
          290   295   300

Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr
305   310   315   320

Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val
          325   330   335

Lys Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile
          340   345   350

Val Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr
          355   360   365

Ala Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala
          370   375   380

Gln Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met
385   390   395   400

Ser Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu
          405   410   415

Leu Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val
          420   425   430

Ser Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala
          435   440   445

Pro Glu Lys Gln Met Ala Pro
450   455

<210> 36
<211> 1903
<212> DNA
<213> Homo sapiens

<220>

<220> CDS
<222> (116)..(1480)

<400> 36
agtcccggct gcagcacctg ggagaaggca gaccgtgtga gggggcctgt ggccccagcg 60

tgctgtggcc tcggggagtg ggaagtggag gcaggagcct tccttacact cgcc atg   118
                                                                 Met
                                                                  1

agt ttc ctc atc gac tcc agc atc atg att acc tcc cag ata cta ttt   166
Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu Phe
             5   10   15

ttt gga ttt ggg tgg ctt ttc ttc atg cgc caa ttg ttt aaa gac tat   214
Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp Tyr
         20   25   30

gag ata cgt cag tat gtt gta cag gtg atc ttc tcc gtg acg ttt gca   262
Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe Ala
     35   40   45

ttt tct tgc acc atg ttt gag ctc atc atc ttt gaa atc tta gga gta   310
Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly Val
 50   55   60   65

ttg aat agc agc tcc cgt tat ttt cac tgg aaa atg aac ctg tgt gta   358
Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys Val
                 70   75   80

att ctg ctg atc ctg gtt ttc atg gtg cct ttt tac att ggc tat ttt   406
Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr Phe
             85   90   95

att gtg agc aat atc cga cta ctg cat aaa caa cga ctg ctt ttt tcc   454
Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe Ser
         100   105   110

tgt ctc tta tgg ctg acc ttt atg tat ttc ttc tgg aaa cta gga gat   502
Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly Asp
     115   120   125

ccc ttt ccc att ctc agc cca aaa cat ggg atc tta tcc ata gaa cag   550
Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu Gln
130   135   140   145

ctc atc agc cgg gtt ggt gtg att gga gtg act ctc atg gct ctt ctt   598
Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu
                 150   155   160

tct gga ttt ggt gct gtc aac tgc cca tac act tac atg tct tac ttc   646
Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe
             165   170   175

ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg   694
Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu
         180   185   190

49

```
ctg caa acc atg gat atg atc ata agc aaa aag aaa agg atg gca atg    742
Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met
    195             200             205

gca cgg aga aca atg ttc cag aag ggg gaa gtg cat aac aaa cca tca    790
Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser
210             215             220             225

ggt ttc tgg gga atg ata aaa agt gtt acc act tca gca tca gga agt    838
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly Ser
            230             235             240

gaa aat ctt act ctt att caa cag gaa gtg gat gct ttg gaa gaa tta    886
Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu Leu
            245             250             255

agc agg cag ctt ttt ctg gaa aca gct gat cta tat gct acc aag gag    934
Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys Glu
            260             265             270

aga ata gaa tac tcc aaa acc ttc aag ggg aaa tat ttt aat ttt ctt    982
Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe Leu
            275             280             285

ggt tac ttt ttc tct att tac tgt gtt tgg aaa att ttc atg gct acc   1030
Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala Thr
290             295             300             305

atc aat att gtt ttt gat cga gtt ggg aaa acg gat cct gtc aca aga   1078
Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr Arg
            310             315             320

ggc att gag atc act gtg aat tat ctg gga atc caa ttt gat gtg aag   1126
Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val Lys
            325             330             335

ttt tgg tcc caa cac att tcc ttc att ctt gtt gga ata atc atc gtc   1174
Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile Val
            340             345             350

aca tcc atc aga gga ttg ctg atc act ctt acc aag ttc ttt tat gcc   1222
Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr Ala
            355             360             365

atc tct agc agt aag tcc tcc aat gtc att gtc ctg cta tta gca cag   1270
Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala Gln
370             375             380             385

ata atg ggc atg tac ttt gtc tcc tct gtg ctg ctg atc cga atg agt   1318
Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser
            390             395             400

atg cct tta gaa tac cgc acc ata atc act gaa gtc ctt gga gaa ctg   1366
Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu
            405             410             415
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50

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cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc   1414
Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser
        420             425             430

gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca   1462
Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro
        435             440             445

gag aag caa atg gca cct tgaacttaag cctactacag actgttagag          1510
Glu Lys Gln Met Ala Pro
450             455

gccagtggtt tcaaaattta gatataagag gggggaaaaa tggaaccagg gcctgacatt 1570

ttataaacaa acaaaatgct atggtagcat ttttcacctt catagcatac tccttccccg 1630

tcaggtgata ctatgaccat gagtagcatc agccagaaca tgagagggag aactaactca 1690

agacaatact cagcagagag catcccgtgt ggatatgagg ctggtgtaga ggcggagagg 1750

agccaagaaa ctaaaggtga aaaatacact ggaactctgg ggcaagacat gtctatggta 1810

gctgagccaa acacgtagga tttccgtttt aaggttcaca tggaaaaggt tatagctttg 1870

ccttgagatt gactcattaa aatcagagac tgt                              1903


<210> 37
<211> 322
<212> PRT
<213> Homo sapiens

<400> 37
Met Ser Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser
 1               5                  10                  15

Ser Ser Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala
            20                  25                  30

Gly Ala Ala Asp Lys Ser Ala Val Val Ala Ala Ala Pro Ala Ser
            35                  40                  45

Val Ala Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile
    50                  55                  60

Ile Ser Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser
65                  70                  75                  80

His Tyr Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met
                85                  90                  95

Met Gly Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala
            100                 105                 110

Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp
        115                 120                 125
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51

```
Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu
    130                 135                 140

Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu
145                 150                 155                 160

Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val
                165                 170                 175

Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp
            180                 185                 190

Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe
            195                 200                 205

Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr
    210                 215                 220

Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu
225                 230                 235                 240

Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly
                245                 250                 255

Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg      .
            260                 265                 270

Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His
            275                 280                 285

Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser
    290                 295                 300

Ala Ala Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp
305                 310                 315                 320

Phe Gln


<210> 38
<211> 1448
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (292)..(1257)

<400> 38
tactgctggc ggctggagcg gagcgcaccg cggcggtggt gcccagagcg gagcgcagct 60

ccctgccccg cccctccccc tcggcctcgc ggcgacggcg gcggtggcgg cttggacgac 120

tcggagagcc gagtgaagac atttccacct ggacacctga ccatgtgcct gccctgagca 180
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52

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                                                              tcggcagttg gcaggctccc tctgcagtgg ggtctgggcc tcggccccac c atg tcg  297
                                                                                                            Met Ser
                                                                                                              1

agc ctc ggc ggt ggc tcc cag gat gcc ggc ggc agt agc agc agc agc  345
Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser Ser Ser
         5                   10                  15

acc aat ggc agc ggt ggc agt ggc agc agt ggc cca aag gca gga gca  393
Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala
    20                  25                  30

gca gac aag agt gca gtg gtg gct gcc gcc gca cca gcc tca gtg gca  441
Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser Val Ala
35                  40                  45                  50

gat gac aca cca ccc ccc gag cgt cgg aac aag agc ggt atc atc agt  489
Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile Ile Ser
                55                  60                  65

gag ccc ctc aac aag agc ctg cgc cgc tcc cgc ccg ctc tcc cac tac  537
Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser His Tyr
                70                  75                  80

tct tct ttt ggc agc agt ggt ggt agt ggc ggt ggc agc atg atg ggc  585
Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met Met Gly
         85                  90                  95

gga gag tct gct gac aag gcc act gcg gct gca gcc gct gcc tcc ctg  633
Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ser Leu
    100                 105                 110

ttg gcc aat ggg cat gac ctg gcg gcg gcc atg gcg gtg gac aaa agc  681
Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser
115                 120                 125                 130

aac cct acc tca aag cac aaa agt ggt gct gtg gcc agc ctg ctg agc  729
Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser
                135                 140                 145

aag gca gag cgg gcc acg gag ctg gca gcc gag gga cag ctg acg ctg  777
Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu
                150                 155                 160

cag cag ttt gcg cag tcc aca gag atg ctg aag cgc gtg gtg cag gag  825
Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu
         165                 170                 175

cat ctc ccg ctg atg agc gag gcg ggt gct ggc ctg cct gac atg gag  873
His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu
    180                 185                 190

gct gtg gca ggt gcc gaa gcc ctc aat ggc cag tcc gac ttc ccc tac  921
Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr
195                 200                 205                 210
```

```
ctg ggc gct ttc ccc atc aac cca ggc ctc ttc att atg acc ccg gca    969
Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala
                215                 220                 225

ggt gtg ttc ctg gcc gag agc gcg ctg cac atg gcg ggc ctg gct gag   1017
Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu
                230                 235                 240

tac ccc atg cag gga gag ctg gcc tct gcc atc agc tcc ggc aag aag   1065
Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys
                245                 250                 255

aag cgg aaa cgc tgc ggc atg tgc gcg ccc tgc cgg cgg cgc atc aac   1113
Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn
            260                 265                 270

tgc gag cag tgc agc agt tgt agg aat cga aag act ggc cat cag att   1161
Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile
275                 280                 285                 290

tgc aaa ttc aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct   1209
Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala
                295                 300                 305

ctg gag aag gtg atg ctt ccg acg gga gcc gcc ttc cgg tgg ttt cag   1257
Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln
                310                 315                 320

tgacggcggc ggaacccaaa gctgccctct ccgtgcaatg tcactgctcg tgtggtctcc 1317

agcaagggat tcgggcgaag acaaacggat gcacccgtct ttagaaccaa aaatattctc 1377

tcacagattt cattcctgtt tttatatata tattttttgt tgtcgtttta acatctccac 1437

gtccctagca t                                                      1448


<210> 39
<211> 313
<212> PRT
<213> Homo sapiens

<400> 39
Met Ala Gly Gln Pro Gly His Met Pro His Gly Gly Ser Ser Asn Asn
 1               5                  10                  15

Leu Cys His Thr Leu Gly Pro Val His Pro Pro Asp Pro Gln Arg His
            20                  25                  30

Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu
            35                  40                  45

Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys
    50                  55                  60

Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu
```

54

Met Met Asp Ala Lys Ala Arg Gln Asp Cys Val Lys Glu Ile Gly Leu
            85   90   95

Leu Lys Gln Leu Asn His Pro Asn Ile Ile Lys Tyr Leu Asp Ser Phe
           100   105   110

Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu Ala Asp Ala Gly
           115   120   125

Asp Leu Ser Gln Met Ile Lys Tyr Phe Lys Lys Gln Lys Arg Leu Ile
130   135   140

Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu Cys Ser Ala Val
145   150   155   160

Glu His Met His Ser Arg Arg Val Met His Arg Asp Ile Lys Pro Ala
           165   170   175

Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu Gly Asp Leu Gly
           180   185   190

Leu Gly Arg Phe Phe Ser Ser Glu Thr Thr Ala Ala His Ser Leu Val
           195   200   205

Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly Tyr
       210   215   220

Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu Met
225   230   235   240

Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Phe Ser
           245   250   255

Leu Cys Gln Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Gly Glu
           260   265   270

His Tyr Ser Glu Lys Leu Arg Glu Leu Val Ser Met Cys Ile Cys Pro
           275   280   285

Asp Pro His Gln Arg Pro Asp Ile Gly Tyr Val His Gln Val Ala Lys
       290   295   300

Gln Met His Ile Trp Met Ser Ser Thr
305   310

<210> 40
<211> 1597
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (153)..(1091)

```
ggcggaaccg agctgacggg cgtgcggccg ctgcgccgca aactcgtgtg ggacgcaccg 60

ctccagccgc ccgcgggcca gcgcaccggt cccccagcgg cagccgagcc cgcccgcgcg 120

ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac    173
                                     Met Ala Gly Gln Pro Gly His
                                      1               5

atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct    221
Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro
         10              15                  20

gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc    269
Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg
     25              30                  35

tgc tcg ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag    317
Cys Ser Leu Ala Asp Phe Gln Ile Glu Lys Lys Ile Gly Arg Gly Gln
 40              45              50                          55

ttc agc gag gtg tac aag gcc acc tgc ctg ctg gac agg aag aca gtg    365
Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val
                 60                  65                  70

gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg    413
Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg
             75                  80                  85

cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca    461
Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro
             90                  95                 100

aat atc atc aag tat ttg gac tcg ttt atc gaa gac aac gag ctg aac    509
Asn Ile Ile Lys Tyr Leu Asp Ser Phe Ile Glu Asp Asn Glu Leu Asn
     105                 110                 115

att gtg ctg gag ttg gct gac gca ggg gac ctc tcg cag atg atc aag    557
Ile Val Leu Glu Leu Ala Asp Ala Gly Asp Leu Ser Gln Met Ile Lys
120                 125                 130                 135

tac ttt aag aag cag aag cgg ctc atc ccg gag agg aca gta tgg aag    605
Tyr Phe Lys Lys Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys
                 140                 145                 150

tac ttt gtg cag ctg tgc agc gcc gtg gag cac atg cat tca cgc cgg    653
Tyr Phe Val Gln Leu Cys Ser Ala Val Glu His Met His Ser Arg Arg
                 155                 160                 165

gtg atg cac cga gac atc aag cct gcc aac gtg ttc atc aca gcc acg    701
Val Met His Arg Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr
         170                 175                 180

ggc gtc gtg aag ctc ggt gac ctt ggt ctg ggc cgc ttc ttc agc tct    749
Gly Val Val Lys Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser
     185                 190                 195
```

56

```
gag acc acc gca gcc cac tcc cta gtg ggg acg ccc tac tac atg tca    797
Glu Thr Thr Ala Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser
200                     205             210                 215

ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg    845
Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp
                220             225             230

tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc    893
Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe
            235             240             245

tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag    941
Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln
        250             255             260

tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga    989
Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg
    265             270             275

gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac   1037
Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp
280             285             290             295

atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc   1085
Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser
                300             305             310

agc acc tgagcgtgga tgcaccgtgc cttatcaaag ccagcaccac tttgccttac   1141
Ser Thr

ttgagtcgtc ttctcttcga gtggccacct ggtagcctag aacagctaag accacagggt 1201

tcagcaggtt ccccaaaagg ctgcccagcc ttacagcaga tgctgaaggc agagcagctg 1261

agggaggggc gctggccaca tgtcactgat ggtcagattc caaagtcctt tctttatact 1321

gttgtggaca atctcagctg ggtcaataag ggcaggtggt tcagcgagcc acggcagccc 1381

cctgtatctg gattgtaatg tgaatcttta gggtaattcc tccagtgacc tgtcaaggct 1441

tatgctaaca ggagacttgc aggagaccgt gtgatttgtg tagtgagcct ttgaaaatgg 1501

ttagtaccgg gttcagttta gttcttggta tcttttcaat caagctgtgt gcttaattta 1561

ctctgttgta aagggataaa gtggaaatca tttttt                          1597


<210> 41
<211> 371
<212> PRT
<213> Homo sapiens

<400> 41
Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro
  1               5                  10                  15
```

57

```
  —    ― ― Pro―Asn Pro Gly Tyr Pro― Gly Gly Pro― Gln Pro Pro―Met Pro Pro―Tyr        ―    ――   ――    ―
                20               25            30
```

```
Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln
        35               40               45
```

```
Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr
    50                   55               60
```

```
Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro
65                   70               75                   80
```

```
Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln
                85               90               95
```

```
Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn
            100              105              110
```

```
Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro
        115              120              125
```

```
Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn
    130              135              140
```

```
Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala
145              150              155              160
```

```
Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr
            165              170              175
```

```
Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe
            180              185              190
```

```
Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe
        195              200              205
```

```
Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His
    210              215              220
```

```
Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr
225              230              235              240
```

```
Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met
            245              250              255
```

```
Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser
            260              265              270
```

```
Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val
        275              280              285
```

```
Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
        290              295              300
```

```
Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe
305              310              315              320
```

58

```
     Thr  Cys  Phe  Leu  Ala  Val  Asp  Thr  Gln  Leu  Leu  Leu  Gly  Asn  Lys  Gln
                          325                           330                          335

     Leu  Ser  Leu  Ser  Pro  Glu  Glu  Tyr  Val  Phe  Ala  Ala  Leu  Asn  Leu  Tyr
                          340                           345                          350

     Thr  Asp  Ile  Ile  Asn  Ile  Phe  Leu  Tyr  Ile  Leu  Thr  Ile  Ile  Gly  Arg
                355                           360                           365

     Ala  Lys  Glu
                370
```

<210> 42
<211> 1781
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (91)..(1203)

<400> 42

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attggccatc accgcgcggc cgcgcagcgg acaccgtgcg taccggcctg cggcgcccgg  60

ccaccggggc ggaccgcgga acccgaggcc atg tcc cat gaa aag agt ttt ttg  114
                                  Met Ser His Glu Lys Ser Phe Leu
                                   1                   5

gtg tct ggg gac aac tat cct ccc ccc aac cct gga tat ccg ggg ggg  162
Val Ser Gly Asp Asn Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly
     10                  15                  20

ccc cag cca ccc atg ccc ccc tat gct cag cct ccc tac cct ggg gcc  210
Pro Gln Pro Pro Met Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala
 25                  30                  35                  40

cct tac cca cag ccc cct ttc cag ccc tcc ccc tac ggt cag cca ggg  258
Pro Tyr Pro Gln Pro Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly
                 45                  50                  55

tac ccc cat ggc ccc agc ccc tac ccc caa ggg ggc tac cca cag ggt  306
Tyr Pro His Gly Pro Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly
             60                  65                  70

ccc tac ccc caa ggg ggc tac cca cag ggc ccc tac cca caa gag ggc  354
Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly
             75                  80                  85

tac cca cag ggc ccc tac ccc caa ggg ggc tac ccc cag ggg cca tat  402
Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr
     90                  95                  100

ccc cag agc ccc ttc ccc ccc aac ccc tat gga cag cca cag gtc ttc  450
Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe
105                  110                  115                  120
```

```
cca gga caa gac cct gac tca ccc cag cat gga aac tac cag gag gag    498
Pro Gly Gln Asp Pro Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu
            125             130             135

ggt ccc cca tcc tac tat gac aac cag gac ttc cct gcc acc aac tgg    546
Gly Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp
            140             145             150

gat gac aag agc atc cga cag gcc ttc atc cgc aag gtg ttc cta gtg    594
Asp Asp Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val
            155             160             165

ctg acc ttg cag ctg tcg gtg acc ctg tcc acg gtg tct gtg ttc act    642
Leu Thr Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr
        170             175             180

ttt gtt gcg gag gtg aag ggc ttt gtc cgg gag aat gtc tgg acc tac    690
Phe Val Ala Glu Val Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr
185             190             195             200

tat gtc tcc tat gct gtc ttc ttc atc tct ctc atc gtc ctc agc tgt    738
Tyr Val Ser Tyr Ala Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys
            205             210             215

tgt ggg gac ttc cgg cga aag cac ccc tgg aac ctt gtt gca ctg tcg    786
Cys Gly Asp Phe Arg Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser
            220             225             230

gtc ctg acc gcc agc ctg tcg tac atg gtg ggg atg atc gcc agc ttc    834
Val Leu Thr Ala Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe
        235             240             245

tac aac acc gag gca gtc atc atg gcc gtg ggc atc acc aca gcc gtc    882
Tyr Asn Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val
        250             255             260

tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc    930
Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr
265             270             275             280

tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc    978
Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe
            285             290             295

gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac    1026
Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr
            300             305             310

gcc tca ctg ggc gct ctg ctc ttc acc tgc ttc ctc gca gtg gac acc    1074
Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr
            315             320             325

cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat    1122
Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr
            330             335             340

gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg    1170
```

60

```
Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu
345             350             355             360

tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgct 1223
Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu
                365                 370

gtgcccgctc aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg 1283

tacttcccct ctctcttgtc cccaggcaca gcctagggaa aaggatgcct ctctccaacc 1343

ctcctgtatg tacactgcag atacttccat ttggacccgc tgtggccaca gcatggcccc 1403

tttagtcctc ccgccccgc caaggggcag caaggccacg tttccgtgcc acctcctgtc 1463

tactcattgt tgcatgagcc ctgtctgcca gcccacccca gggactgggg gcagcaccag 1523

gtcccgggga gagggattga gccaagaggt gagggtgcac gtcttccctc ctgtcccagc 1583

tccccagcct ggcgtagagc acccctcccc tcccccccac ccccctggag tgctgccctc 1643

tggggacatg cggagtgggg gtcttatccc tgtgctgagc cctgagggca gagaggatgg 1703

catgtttcag gggaggggga agccttcctc tcaatttgtt gtcagtgaaa ttccaataaa 1763

tgggatttgc tctctgcc                                              1781
```

<210> 43
<211> 393
<212> PRT
<213> Homo sapiens

<400> 43

```
Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala
 1               5                   10                  15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
            20              25                  30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
        35                  40                  45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
    50                  55                  60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
65                  70                  75                  80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg
                85                  90                  95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
            100             105                 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
        115                 120                 125
```

61

```
Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
    130                 135                 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
145                 150                 155                 160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
                165                 170                 175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
            180                 185                 190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
        195                 200                 205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
    210                 215                 220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
225                 230                 235                 240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
            245                 250                 255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
            260                 265                 270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
    275                 280                 285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr
    290                 295                 300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn
305                 310                 315                 320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu
            325                 330                 335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly
            340                 345                 350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala
        355                 360                 365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu
    370                 375                 380

Leu Val Pro Gly Pro Glu Lys Glu Asn
385                 390


<210> 44
<211> 2396
<212> DNA
<213> Homo sapiens


                                    62
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<220>
<221> CDS
<222> (50)..(1228)

<400> 44
agctgtgcac tctccatcca gctgtgcgct ctcgtcggga gtcccagcc atg tcc gac 58
                                                       Met Ser Asp
                                                        1

gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg   106
Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro
        5   10   15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc   154
Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser
 20   25   30   35

gaa ggg gcc gcc gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta   202
Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu
                40   45   50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg   250
Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg
                55   60   65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg   298
Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu
            70   75   80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg   346
Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu
        85   90   95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg   394
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
100   105   110   115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga   442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
                120   125   130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg   490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
                135   140   145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt   538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
                150   155   160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc   586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
        165   170   175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac   634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
180   185   190   195

63

```
atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca    682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr
                200             205                 210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag    730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu
                215             220                 225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act    778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr
                230             235                 240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att    826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile
                245             250                 255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc    874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu
260                 265                 270                 275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg    922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu
                280             285                 290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat    970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn
                295             300                 305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg    1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val
                310             315                 320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt    1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser
                325             330                 335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag    1114
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
340                 345             350                 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg    1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
                360             365                 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca    1210
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
                375             380                 385

ggg cca gag aag gag aac tagggcaagt ggctgtgaga ccctagagac          1258
Gly Pro Glu Lys Glu Asn
            390

cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318

ctgtcataat gctctgccct ccctccccg aagttctctg tggtgatgac cgctctcccc 1378
```

```
 —    —      —    tgcccctccc cgcttcctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg 1438
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        ccccgggcct gctgtgctgc ttttgtgcca aggttagcca gtccccctg ttgtgttcca 1558
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        ttgaaacgtc agctcaggat atggggccaa tctctgtgag tccagcatgt acctgtctct 1678
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        gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattcccctt gcagttaggg 2038
        gaggccctac tgccttctca aagcagagag gcagcttatc aaactcagcc caaaactctg 2098
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        ggattaggga gggttattgc cccaaccatt gcaatgggag gtggagggac aggctcagcc 2278
        tcctcattgt ctaaatgagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338
        accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396


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<211> 393
<212> PRT
<213> Homo sapiens

<400> 45
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 1               5                  10                  15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
            20                  25                  30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
        35                  40                  45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
    50                  55                  60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
·65                  70                  75                  80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg
```

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
        100   105   110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
        115   120   125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
130   135   140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
145   150   155   160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
                165   170   175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
                180   185   190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
                195   200   205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
210   215   220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
225   230   235   240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
                245   250   255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
                260   265   270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
        275   280   285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr
        290   295   300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn
305   310   315   320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu
                325   330   335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly
        340   345   350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala
        355   360   365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu
        370   375   380

Leu Val Pro Gly Pro Glu Lys Gln Asn

66

<210> 46
<211> 2396
<212> DNA
<213> Homo sapiens

<220>
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<222> (50)..(1228)

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                                                         Met Ser Asp
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gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg   106
Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro
      5   10   15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc   154
Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser
 20   25   30   35

gaa ggg gcc gcc gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta   202
Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu
                40   45   50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg   250
Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg
                55   60   65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg   298
Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu
            70   75   80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg   346
Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu
        85   90   95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg   394
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
100   105   110   115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga   442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
                120   125   130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg   490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
                135   140   145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt   538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
            150   155   160

67

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gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc       586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
        165             170             175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac       634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
180             185             190             195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca       682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr
                200             205             210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag       730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu
                215             220             225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act       778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr
        230             235             240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att       826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile
        245             250             255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc       874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu
260             265             270             275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg       922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu
                280             285             290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat       970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn
                295             300             305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg      1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val
        310             315             320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt      1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser
        325             330             335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag      1114
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
340             345             350             355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg      1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
                360             365             370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca      1210
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
        375             380             385

ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac           1258
Gly Pro Glu Lys Gln Asn
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68

Gly Pro Glu Lys Gln Asn
          390

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cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318

ctgtcataat gctctgccct ccctcccccg aagttctctg tggtgatgac cgctctcccc 1378

tgcccctccc cgcttcctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg 1438

ccctgccaag gcgacaggga gggtcagagg gaggccggct gcttcctgcc cccacccttt 1498

ccccgggcct gctgtgctgc ttttgtgcca aggttagcca gtcccccctg ttgtgttcca 1558

tgtgctttca cctctgcctc atctttcctc ccgtccctgc cccgccacct ccccaaagaa 1618

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ccctagtgtc ccttcagcct gggctgacca gtgcccgcct ctgggcttga ccagttccca 1738

atctcgtcct ctgtccccaa cttcttaagc acaattgggc ttcttccatc tccaggtttt 1798

ctgccattct taaccaaggc agccccaagc ctcctgggga ggcagggcaa aaacaggtgc 1858

cctcatcgtg gtctgtgcca tgtcccgtct ctatggtggt tgaggagaaa ggcgggggaag 1918

cttcctcagc cttgcagata tgtgtggcat ttactagcca gagctctgaa aggcagtgct 1978

gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattcccctt gcagttaggg 2038

gaggccctac tgccttctca aagcagagag gcagcttatc aaactcagcc caaaactctg 2098

tttacatggg tggggagatg gagcagggaa gtacagagtg ggatggtcag gacctgggcc 2158

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ggattaggga gggttattgc cccaaccatt gcaatgggag gtggagggac aggctcagcc 2278

tcctcattgt ctaaatgagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338

accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg    2396
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<210> 47
<211> 138
<212> PRT
<213> Homo sapiens

<400> 47
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Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly
1               5                  10                  15

Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys
            20                  25                  30

Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe
        35                  40                  45
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69

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    Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys
        50                      55              60

    Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile
    65                      70              75                      80

    Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu
                    85                      90                  95

    Leu Phe Arg Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val
                    100             105             110

    Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val
                115             120             125

    Asp Lys Val Gly Glu Ser Asn Asn Met Val
        130             135
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<210> 48
<211> 2976
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (110)..(523)

<400> 48
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accctgggct ttccgaggtg ctgtcgccgc tgtccccacc actgcagcc atg atc tcc 118
                                                      Met Ile Ser
                                                        1

tta acg gac acg cag aaa att gga atg gga tta aca gga ttt gga gtg   166
Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly Phe Gly Val
      5                      10                  15

ttt ttc ctg ttc ttt gga atg att ctc ttt ttt gac aaa gca cta ctg   214
Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys Ala Leu Leu
 20                      25                  30                  35

gct att gga aat gtt tta ttt gta gcc ggc ttg gct ttt gta att ggt   262
Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe Val Ile Gly
                40                      45                  50

tta gaa aga aca ttc aga ttc ttc ttc caa aaa cat aaa atg aaa gct   310
Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys Met Lys Ala
                55                      60                  65

aca ggt ttt ttt ctg ggt ggt gta ttt gta gtc ctt att ggt tgg cct   358
Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile Gly Trp Pro
            70                      75                  80

ttg ata ggc atg atc ttc gaa att tat gga ttt ttt ctc ttg ttc agg   406
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Leu_Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Leu Phe Arg
    85                      90                  95

ggc ttc ttt cct gtc gtt gtt ggc ttt att aga aga gtg cca gtc ctt    454
Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu
100                     105                 110                 115

gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt    502
Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val
                    120                 125                 130

gga gaa agc aac aat atg gta taacaacaag tgaatttgaa gactcattta       553
Gly Glu Ser Asn Asn Met Val
                135

aaatattgtg ttatttataa agtcatttga agaatattca gcacaaaatt aaattacatg 613

aaatagcttg taatgttctt tacaggagtt taaaacgtat agcctacaaa gtaccagcag 673

caaattagca aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 733

caagcaaact gagagaggtg aaatccatgt taatgatgct taagaaactc ttgaaggcta 793

tttgtgttgt ttttccacaa tgtgcgaaac tcagccatcc ttagagaact gtggtgcctg 853

tttcttttct ttttattttg aaggctcagg agcatccata ggcatttgct ttttagaaat 913

gtccactgca atggcaaaaa tatttccagt tgcactgtat ctctggaagt gatgcatgaa 973

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ggattacttt tttttgtaaa catggttaaa ataaaacttc tgtggttctt ctgaatctta 1093

atatttcaaa gccaggtgaa aatctgaact agatattctt tgttggaata tgcaaaggtc 1153

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tgtaagtatt taacaaaaaa gcattcttga ccatgaatga agtagtttgt ttcatagctt 1333

gtctcattga atagtattat tgaagatact aaatgatgca aaccaaatgg attttttcca 1393

tgtcatgatg taattttttct ttcttctttc tttttttttaa attttagcag tggcttatta 1453

tttgtttttc ataaattaaa ataacttttg ataatgttta ctttaagaca tgtaacatgt 1513

taaaaggtta aacttatggc tgttttttaaa gggctattca tttaatctga gttttcccctt 1573

attttcagct ttttcctagc atataatagt cattaagcat gacatatcct tcatatgatc 1633

actcatcttg agttaattag aaaatacctg agttcacgtg ctaaagtcat ttcactgtaa 1693

taaactgact atggtttctt aagaacatga cactaaaaaa aaagtggttt ttttccaccg 1753

ttgctgatta ttagacagta ggaaatagct gttttctttta gttttacaag atgtgacagc 1813
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71

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tttagtggta gatgtaggga aacatttcaa cagccatagt actatttgtt ttaccactga 1873

ttgcactgtt ttgttttttt aacagttgca aagctttta atgcataaaa gtataattga 1933

aatctgtggt atttatttac aaacatgtct acaaaaatag attacagctt attttatttt 1993

tagttaaatc tcttaataca cagagaactc ccaatcttgc tcatctaaat aaggaaagac 2053

ttggtgtata gtgtgatggt ttagtcttaa ggattaagac attttttggta cttgcatttg 2113

acttacgatg tatctgtgaa aatgggatga tattgacaaa tggagactcc tacctcaata 2173

gttaatggaa taataagagg ctactgttgt gtctaatgtt cttcaaaaaa gtaatatcct 2233

cacttggaga gtgtcaaata catactttga ggattgactt tatataaggt gccctgtaga 2293

actctgttac acatatttt gacccatatt atttacaatg tcttgataat tctacctttt 2353

tagagcaaga atagtatctg ctaatgtaag ggacatctgt atttaactcc tttgtagaca 2413

tgaatttcta tcaaaatgtt ctttgcactg taacagagat tcctttttc aataatctta 2473

attcaaaagc attattagac ttgaaagggt ttgataatct cccagtcctt agtaaagatt 2533

gagagaggct ggagcagttt tcagttttaa atgagtctgc agttaatatc aaatgtgagt 2593

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cagccttctg tctgtaacaa aaatgtactt tatagagatg gaggaaaagg tctaatacta 2773

catagcctta agtgtttctg tcattgttca agtgtatttt ctgtaacaga aacatatttg 2833

gaatgttttt cttttcccct tataaattgt aattcctgaa atactgctgc tttaaaaagt 2893

cccactgtca gattatatta tctaacaatt gaatattgta aatatacttg tcttacctct 2953

caataaaagg gtacttttct att                                         2976
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<210> 49
<211> 359
<212> PRT
<213> Homo sapiens

<400> 49

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Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe
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His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln
            20                  25                  30

Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val
        35                  40                  45

Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro
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72

Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met
65   70   75   80

Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile
              85   90   95

Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser
              100   105   110

Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu
        115   120   125

His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp
        130   135   140

Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg
145   150   155   160

Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His
              165   170   175

Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr
              180   185   190

Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu
        195   200   205

Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro
    210   215   220

Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile
225   230   235   240

Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser
              245   250   255

Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser
        260   265   270

Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe
        275   280   285

Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His
    290   295   300

Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met
305   310   315   320

Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser
              325   330   335

Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser
              340   345   350

Arg Ser Thr Thr His Leu Ile

<210> 50
<211> 2636
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (327)..(1403)

<400> 50
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atgttaatat attggcaaca attattcagt tatttcaagt accattggaa gaggaaggac 120

aacgtggtgg acctatcctt gcaccagagg agattaagac tattttggt agcatcccag 180

atatctttga tgtacacact aagataaagg atgatcttga gaccttata gttaattggg 240

atgagagcaa aagcattggt gacattttc tgaaatattc aaaagatttg gtaaaaacct 300

accctccctt tgtaaacttc tttgaa atg agc aag gaa aca att att aaa tgt 353
                                Met Ser Lys Glu Thr Ile Ile Lys Cys
                                 1   5

gaa aaa cag aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca   401
Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala
 10   15   20   25

aaa cca gaa tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca   449
Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro
                30   35   40   .

gta cag agg tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag   497
Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys
                45   50   55

cat aca gct gat gaa aat cca gac aaa agc act tta gaa aaa gct att   545
His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile
            60   65   70

gga tca ctg aag gaa gta atg acg cat att aat gag gat aag aga aaa   593
Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys
     75   80   85

aca gaa gct caa aag caa att ttt gat gtt gtt tat gaa gta gat gga   641
Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly
 90   95   100   105

tgc cca gct aat ctt tta tct tct cac cga agc tta gta cag cgg gtt   689
Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val
                110   115   120

gaa aca att tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta   737
Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val

```
act ctc ttc ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac    785
Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His
        140             145             150

aag gtt att ggc act ttt agg agt cct cat ggc caa acc cga ccc cca    833
Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro
        155             160             165

gct tct ctt aag cat att cac cta atg cct ctt tct cag att aag aag    881
Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys
170             175             180             185

gta ttg gac ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg    929
Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu
                190             195             200

ctt gtg agg cca cca aca gag cag gca aat gtg cta ctc agt ttc cag    977
Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln
            205             210             215

atg aca tca gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt   1025
Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys
        220             225             230

cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att   1073
Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile
        235             240             245

tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac   1121
Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp
250             255             260             265

agt aca ttg agt aga gca tca aga gca ata aaa aag act tca aaa aag   1169
Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys
            270             275             280

gtt aca aga gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga   1217
Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg
            285             290             295

agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc   1265
Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser
        300             305             310

agc aat gat aag cat gta atg agt cgt ctt tct agc aca tca tca tta   1313
Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu
        315             320             325

gca ggt atc cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa   1361
Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu
330             335             340             345

agg aga agt cat acg tta agt aga tct aca act cat ttg ata          1403
Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His Leu Ile
            350             355
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75

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tgaagcgtta ccaaaatctt aaattataga aatgtataga cacctcatac tcaaataaga 1463

aactgactta aatggtactt gtaattagca cttggtgaaa gctggaagga agataaataa 1523

cactaaacta tgctatttga tttttcttct tgaaagagta aggtttacct gttacatttt 1583

caagttaatt catgtaaaaa atgatagtga ttttgatgta atttatctct tgtttgaatc 1643

tgtcattcaa aggccaataa tttaagttgc tatcagctga tattagtagc tttgcaaccc 1703

tgatagagta aataaatttt atgggcgggt gccaaatact gctgtgaatc tatttgtata 1763

gtatccatga atgaatttat ggaaatagat atttgtgcag ctcaatttat gcagagatta 1823

aatgacatca taatactgga tgaaaacttg catagaattc tgattaaata gtgggtctgt 1883

ttcacatgtg cagtttgaag tatttaaata accactcctt tcacagttta ttttcttctc 1943

aagcgttttc aagatctagc atgtggattt taaaagattt gccctcatta acaagaataa 2003

catttaaagg agattgtttc aaaatatttt tgcaaattga dataaggaca gaaagattga 2063

gaaacattgt atattttgca aaaacaagat gtttgtagct gtttcagaga gagtacggta 2123

tatttatggt aattttatcc actagcaaat cttgatttag tttgatagtg tgtggaattt 2183

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gttcaacttt ttattgtggt cttataatta aatgtaaaat tgaaaattca tttgctgttt 2363

caaagtgtga tatctttcac aatagccttt ttatagtcag taattcagaa taatcaagtt 2423

catatggata aatgcatttt tatttcctat ttctttaggg agtgctacaa atgtttgtca 2483

cttaaatttc aagtttctgt tttaatagtt aactgactat agattgtttt ctatgccatg 2543

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<210> 51
<211> 883
<212> PRT
<213> Homo sapiens

<400> 51

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Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu
            20                  25                  30

Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln
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76

Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu
    50   55   60

Leu Thr Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu
65   70   75   80

Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val
            85   90   95

Phe Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys
          100   105   110

Ala Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln
         115   120   125

Lys Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser
        130   135   140

Met Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu
145   150   155   160

Leu Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg
         165   170   175

Lys Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln
        180   185   190

Gly Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys
        195   200   205

Pro Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe
      210   215   220

Tyr Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe
225   230   235   240

Gln Asp Cys Ile Phe Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr
        245   250   255

Asn Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu
        260   265   270

Gly Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys
        275   280   285

Asp Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu
        290   295   300

Trp Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met
305   310   315   320

Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser
        325   330   335

Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu

77

Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe
    355   360   365

Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser
    370   375   380

Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp
385   390   395   400

Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro
          405   410   415

Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr
          420   425   430

Glu Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln
          435   440   445

Val Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro
          450   455   460

Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val
465   470   475   480

His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp
          485   490   495

Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu
          500   505   510

Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu
          515   520   525

Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu
          530   535   540

Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu
545   550   555   560

Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu
          565   570   575

Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr
          580   585   590

Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn
          595   600   605

Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val
          610   615   620

Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser
625   630   635   640

Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp

78

Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile
       660   665   670

Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly
       675   680   685

Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His Leu Met Pro Leu
  690   695   700

Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His
705   710   715   720

Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val
          725   730   735

Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp
      740   745   750

Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp
      755   760   765

Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn
  770   775   780

Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys
785   790   795   800

Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro
          805   810   815

Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His Gly Ser Val Glu
       820   825   830

Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met Ser Arg Leu Ser
      835   840   845

Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu
  850   855   860

Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr
865   870   875   880

His Leu Ile

<210> 52
<211> 3910
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
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                                  1               5


tcc act act ggg agg act agc ttg gca gac tct tcc att ttt gat tct        100
Ser Thr Thr Gly Arg Thr Ser Leu Ala Asp Ser Ser Ile Phe Asp Ser
    10                  15                  20


aaa gtt act gag att tcc aag gaa aac tta ctt att gga tct act tca        148
Lys Val Thr Glu Ile Ser Lys Glu Asn Leu Leu Ile Gly Ser Thr Ser
25                  30                  35                  40


tat gta gaa gaa gag atg cct cag att gaa aca aga gtg ata ttg gtt        196
Tyr Val Glu Glu Glu Met Pro Gln Ile Glu Thr Arg Val Ile Leu Val
                45                  50                  55


caa gaa gct gga aaa caa gaa gaa ctt aca aaa gcc tta aag gac att        244
Gln Glu Ala Gly Lys Gln Glu Glu Leu Thr Lys Ala Leu Lys Asp Ile
            60                  65                  70


aaa gtg ggc ttt gta aag atg gag tca gtg gaa gaa ttt gaa ggt ttg        292
Lys Val Gly Phe Val Lys Met Glu Ser Val Glu Glu Phe Glu Gly Leu
            75                  80                  85


gat tct ccg gaa ttt gaa aat gta ttt gta gtc acg gac ttt cag gat        340
Asp Ser Pro Glu Phe Glu Asn Val Phe Val Val Thr Asp Phe Gln Asp
        90                  95                  100


tct gtc ttt aat gac ctc tac aag gct gat tgt aga gtt att gga cca        388
Ser Val Phe Asn Asp Leu Tyr Lys Ala Asp Cys Arg Val Ile Gly Pro
105                 110                 115                 120


cca gtt gta tta aat tgt tca caa aaa gga gag cct ttg cca ttt tca        436
Pro Val Val Leu Asn Cys Ser Gln Lys Gly Glu Pro Leu Pro Phe Ser
                125                 130                 135


tgt cgc ccg ttg tat tgt aca agt atg atg aat cta gta cta tgc ttt        484
Cys Arg Pro Leu Tyr Cys Thr Ser Met Met Asn Leu Val Leu Cys Phe
            140                 145                 150


act gga ttt agg aaa aaa gaa gaa cta gtc agg ttg gtg aca ttg gtc        532
Thr Gly Phe Arg Lys Lys Glu Glu Leu Val Arg Leu Val Thr Leu Val
        155                 160                 165


cat cac atg ggt gga gtt att cga aaa gac ttt aat tca aaa gtt aca        580
His His Met Gly Gly Val Ile Arg Lys Asp Phe Asn Ser Lys Val Thr
    170                 175                 180


cat ttg gtg gca aat tgt aca caa gga gaa aaa ttc agg gtt gct gtg        628
His Leu Val Ala Asn Cys Thr Gln Gly Glu Lys Phe Arg Val Ala Val
185                 190                 195                 200


agt cta ggt act cca att atg aag cca gaa tgg att tat aaa gct tgg        676
Ser Leu Gly Thr Pro Ile Met Lys Pro Glu Trp Ile Tyr Lys Ala Trp
                205                 210                 215
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gaa agg cgg aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga    724
Glu Arg Arg Asn Glu Gln Asp Phe Tyr Ala Ala Val Asp Asp Phe Arg
            220             225             230

aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg    772
Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu
        235             240             245

gga ttt tca gat gaa gag aaa acc aat atg gaa gaa atg act gaa atg    820
Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met
        250             255             260

caa gga ggt aaa tat tta ccg ctt gga gat gaa aga tgc act cac ctt    868
Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu
265             270             275             280

gta gtt gaa gag aat ata gta aaa gat ctt ccc ttt gaa cct tca aag    916
Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys
            285             290             295

aaa ctt tat gtt gtc aag caa gag tgg ttc tgg gga agc att caa atg    964
Lys Leu Tyr Val Val Lys Gln Glu Trp Phe Trp Gly Ser Ile Gln Met
            300             305             310

gat gcc cga gct gga gaa act atg tat tta tat gaa aag gca aat act   1012
Asp Ala Arg Ala Gly Glu Thr Met Tyr Leu Tyr Glu Lys Ala Asn Thr
            315             320             325

cct gag ctc aag aaa tca gtg tca atg ctt tct cta aat acc cct aac   1060
Pro Glu Leu Lys Lys Ser Val Ser Met Leu Ser Leu Asn Thr Pro Asn
        330             335             340

agc aat cgc aaa cga cgt cgt tta aaa gaa aca ctt gct cag ctt tca   1108
Ser Asn Arg Lys Arg Arg Arg Leu Lys Glu Thr Leu Ala Gln Leu Ser
345             350             355             360

aga gat aca gac gtg tca cca ttt cca ccc cgt aag cgc cca tca gct   1156
Arg Asp Thr Asp Val Ser Pro Phe Pro Pro Arg Lys Arg Pro Ser Ala
            365             370             375

gag cat tcc ctt tcc ata ggg tca ctc cta gat atc tcc aac aca cca   1204
Glu His Ser Leu Ser Ile Gly Ser Leu Leu Asp Ile Ser Asn Thr Pro
            380             385             390

gag tct agc att aac tat gga gac acc cca aag tct tgt act aag tct   1252
Glu Ser Ser Ile Asn Tyr Gly Asp Thr Pro Lys Ser Cys Thr Lys Ser
            395             400             405

tct aaa agc tcc act cca gtt cct tca aag cag tca gca agg tgg caa   1300
Ser Lys Ser Ser Thr Pro Val Pro Ser Lys Gln Ser Ala Arg Trp Gln
        410             415             420

gtt gca aaa gag ctt tat caa act gaa agt aat tat gtt aat ata ttg   1348
Val Ala Lys Glu Leu Tyr Gln Thr Glu Ser Asn Tyr Val Asn Ile Leu
425             430             435             440

gca aca att att cag tta ttt caa gta cca ttg gaa gag gaa gga caa   1396
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          Ala  Thr Ile Ile Gln Leu Phe Gln Val Pro Leu Glu Glu Glu Gly Gln
                       445               450               455

          cgt ggt gga cct atc ctt gca cca gag gag att aag act att ttt ggt   1444
          Arg Gly Gly Pro Ile Leu Ala Pro Glu Glu Ile Lys Thr Ile Phe Gly
                       460               465               470

          agc atc cca gat atc ttt gat gta cac act aag ata aag gat gat ctt   1492
          Ser Ile Pro Asp Ile Phe Asp Val His Thr Lys Ile Lys Asp Asp Leu
                       475               480               485

          gaa gac ctt ata gtt aat tgg gat gag agc aaa agc att ggt gac att   1540
          Glu Asp Leu Ile Val Asn Trp Asp Glu Ser Lys Ser Ile Gly Asp Ile
                       490               495               500

          ttt ctg aaa tat tca aaa gat ttg gta aaa acc tac cct ccc ttt gta   1588
          Phe Leu Lys Tyr Ser Lys Asp Leu Val Lys Thr Tyr Pro Pro Phe Val
          505               510               515               520

          aac ttc ttt gaa atg agc aag gaa aca att att aaa tgt gaa aaa cag   1636
          Asn Phe Phe Glu Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln
                       525               530               535

          aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca aaa cca gaa   1684
          Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu
                       540               545               550

          tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca gta cag agg   1732
          Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg
                       555               560               565

          tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag cat aca gct   1780
          Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala
                       570               575               580

          gat gaa aat cca gac aaa agc act tta gaa aaa gct att gga tca ctg   1828
          Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu
          585               590               595               600

          aag gaa gta atg acg cat att aat gag gat aag aga aaa aca gaa gct   1876
          Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala
                       605               610               615

          caa aag caa att ttt gat gtt gtt tat gaa gta gat gga tgc cca gct   1924
          Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala
                       620               625               630

          aat ctt tta tct tct cac cga agc tta gta cag cgg gtt gaa aca att   1972
          Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile
                       635               640               645

          tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta act ctc ttc   2020
          Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe
                       650               655               660

          ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac aag gtt att   2068
          Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile
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ggc act ttt agg agt cct cat ggc caa acc cga ccc cca gct tct ctt   2116
Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu
            685                 690                 695

aag cat att cac cta atg cct ctt tct cag att aag aag gta ttg gac   2164
Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp
            700                 705                 710

ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg ctt gtg agg   2212
Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg
            715                 720                 725

cca cca aca gag cag gca aat gtg cta ctc agt ttc cag atg aca tca   2260
Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser
    730                 735                 740

gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt cga cat gta   2308
Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val
745                 750                 755                 760

gct aac acc att tgt aaa gca gat gct gag aat ctt att tat act gct   2356
Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala
                765                 770                 775

gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac agt aca ttg   2404
Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu
            780                 785                 790

agt aga gca tca aga gca ata aaa aag act tca aaa aag gtt aca aga   2452
Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg
            795                 800                 805

gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga agg gct ctt   2500
Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu
    810                 815                 820

atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc agc aat gat   2548
Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp
825                 830                 835                 840

aag cat gta atg agt cgt ctt tct agc aca tca tca tta gca ggt atc   2596
Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile
            845                 850                 855

cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa agg aga agt   2644
Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser
            860                 865                 870

cat acg tta agt aga tct aca act cat ttg ata tgaagcgtta ccaaaatctt 2697
His Thr Leu Ser Arg Ser Thr Thr His Leu Ile
            875                 880

aaattataga aatgtataga cacctcatac tcaaataaga aactgactta aatggtactt 2757

gtaattagca cttggtgaaa gctggaagga agataaataa cactaaacta tgctatttga 2817
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tttaagttgc tatcagctga tattagtagc tttgcaaccc tgatagagta aataaatttt 2997

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tatttcctat ttctttaggg agtgctacaa atgtttgtca cttaaatttc aagtttctgt 3777

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<212> PRT
<213> Homo sapiens

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Pro His Pro Pro Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn
            20                  25                  30

Lys Glu Leu Ala Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser
        35                  40                  45

Ser Asn Cys Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg
    50                  55                  60
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84

Cys Lys Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys
65   70   75   80

Glu Asn Val Ser Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp
        85   90   95

Leu Val Lys Phe Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly
        100   105   110

Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His
        115   120   125

Leu Pro Met Val Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu
        130   135   140

Ile Asp Gly Glu Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln
145   150   155   160

His Met Pro Ile Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn
        165   170   175

Met Thr Asp Val Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys
        180   185   190

Val Ile Gly Pro Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser
        195   200   205

Leu Asn Val Val Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala
210   215   220

Val Ala Ala Gly Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly
225   230   235   240

Ser Ser Leu Asp Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met
        245   250   255

Ala Leu Gln Asn Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu
        260   265   270

Ala Lys Met Arg Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln
        275   280   285

Lys Cys Glu Leu Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp
        290   295   300

Ala Ile Gly Tyr Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys
305   310   315   320

Gly Cys Leu Leu Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg
        325   330   335

Phe Leu Val Gly Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu
        340   345   350

Leu Ser Ser Val Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe
        355   360   365

85

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Pro Asp Leu Ala Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile
    370                 375             380

Val Ala Phe Leu Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly
385             390             395                 400

Phe Thr Lys Ala Ser Glu Glu Lys Lys Val Asn Ile Ile Thr Leu
                405             410             415

Ala Glu Thr Gly Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu
            420             425             430

Ile Arg Lys Pro Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys
        435             440             445

Val Ala Arg Tyr Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly
    450             455             460

Phe Gly Asn His His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met
465             470             475             480

Val Cys Gly Trp Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His
            485             490             495

Cys Ala Thr Thr Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln
            500             505             510

Ile Val Ala Cys Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr
        515             520             525

Phe His Phe Ser Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln
    530             535             540

Ile Ala Phe Leu Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys
545             550             555             560

Gln Ser Lys His Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr
            565             570             575


Asn Leu Gly Phe Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys
            580             585             590

Phe Gly Leu Val Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr
        595             600             605

Met Val Phe His Pro Ala Arg Glu Lys Val Leu Arg Ser Val
    610             615             620


<210> 54
<211> 2426
<212> DNA
<213> Homo sapiens

<220>
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86

\<221\> CDS
\<222\> (104)..(1969)

\<400\> 54
gcgccagcag gaagtgggag aagaggcgac ccaaggcggg ctggcgggct ggcggcagtc 60

gctacttgcc tagtagcctc agccgctgtg ggctcctggg gag atg gag ggg ccg 115
                                              Met Glu Gly Pro
                                               1

ggg ctg ggc tcg cag tgc agg aat cac agc cat ggc ccc cac cct cca 163
Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly Pro His Pro Pro
 5   10   15   20

gga ttt ggt cga tat ggc atc tgt gca cat gaa aac aaa gaa ctt gcc 211
Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn Lys Glu Leu Ala
             25   30   35

aat gca aga gaa gct ctt cct ctt ata gag gac tct agt aac tgt gac 259
Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser Ser Asn Cys Asp
         40   45   50

att gtc aaa gct act caa tac gga att ttt gaa cga tgt aaa gag ttg 307
Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg Cys Lys Glu Leu
     55   60   65

gta gaa gca gga tat gat gtc agg caa cca gat aaa gaa aat gtg tcg 355
Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Ser
 70   75   80

ctt ctt cat tgg gct gct att aac aac aga ctg gat ctt gta aag ttt 403
Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp Leu Val Lys Phe
 85   90   95   100

tat att tca aaa ggt gct gtt gta gat cag ttg ggt gga gat tta aat 451
Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly Gly Asp Leu Asn
                 105   110   115

tca act cct ctt cac tgg gcc atc cga caa gga cat tta cct atg gtc 499
Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His Leu Pro Met Val
             120   125   130

ata tta tta ctc cag cat ggt gca gac ccc act ctt att gat gga gag 547
Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu Ile Asp Gly Glu
         135   140   145

gga ttc agc agc atc cac ctg gca gta ttg ttt caa cac atg cct att 595
Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln His Met Pro Ile
 150   155   160

ata gca tat ctc atc tca aag gga cag agt gtg aat atg aca gat gta 643
Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn Met Thr Asp Val
165   170   175   180

aat ggg cag aca cct ctc atg tta tca gct cac aaa gta att ggg cca 691
Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys Val Ile Gly Pro
                 185   190   195

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gaa cca act gga ttt ctt tta aag ttt aat cct tct ctc aat gtg gtt    739
Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser Leu Asn Val Val
            200             205             210

gat aaa ata cac caa aac act cca ctt cac tgg gca gtt gca gca gga    787
Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala Val Ala Ala Gly
            215             220             225

aat gtt aat gca gtt gat aag ctt ttg gaa gct ggt tct agc ctg gat    835
Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly Ser Ser Leu Asp
            230             235             240

atc cag aat gtt aag gga gaa aca cct ctt gat atg gct cta caa aac    883
Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met Ala Leu Gln Asn
245             250             255             260

aaa aat cag ctc att att cat atg cta aaa aca gaa gcc aaa atg aga    931
Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg
            265             270             275

gcc aac caa aag ttc aga ctt tgg agg tgg ctg cag aaa tgc gag ctc    979
Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln Lys Cys Glu Leu
            280             285             290

ttc ctg ctg ctg atg ctt tct gtg att acc atg tgg gct att gga tac   1027
Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp Ala Ile Gly Tyr
            295             300             305

ata ttg gac ttc aat tca gat tct tgg ctt tta aaa gga tgt ctt cta   1075
Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys Gly Cys Leu Leu
310             315             320

gta aca ctg ttt ttt ctg aca tct ttg ttt cca agg ttc ttg gtt ggg   1123
Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg Phe Leu Val Gly
325             330             335             340

tat aag aac ctt gta tac tta cca aca gcc ttt ctg cta agt tct gtt   1171
Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu Leu Ser Ser Val
            345             350             355

ttt tgg ata ttt atg act tgg ttc atc tta ttt ttt cct gat tta gca   1219
Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe Pro Asp Leu Ala
            360             365             370

gga gcc cct ttc tat ttc agt ttc att ttc agc ata gta gcc ttt cta   1267
Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile Val Ala Phe Leu
            375             380             385

tac ttt ttc tat aag act tgg gca act gat cca ggc ttc act aag gct   1315
Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly Phe Thr Lys Ala
            390             395             400

tct gaa gaa gaa aag aaa gtg aat atc atc acc ctt gca gaa act ggc   1363
Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu Ala Glu Thr Gly
405             410             415             420
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_ _ _ _ _ _ _ _ _ tct_ctg_gac_ttc_aga_aca_ttt_tgt_aca_tca_tgt_ctt_ata_agg_aag_cca_ _1411_ _ _ _ _ _ _ _ _
           Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu Ile Arg Lys Pro
                       425             430                 435

           tta agg tca ctc cac tgc cat gta tgc aac tgc tgt gtg gct cga tat    1459
           Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys Val Ala Arg Tyr
                       440             445                 450

           gat caa cac tgc ctg tgg act gga cgg tgc ata ggt ttt ggc aac cat    1507
           Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly Phe Gly Asn His
                       455             460                 465

           cac tat tac ata ttc ttc ttg ttt ttc ctt tcc atg gta tgt ggc tgg    1555
           His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met Val Cys Gly Trp
                470             475                 480

           att ata tat gga tct ttc atc tat ttg tcc agt cat tgt gcc aca aca    1603
           Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His Cys Ala Thr Thr
           485             490                 495                 500

           ttc aaa gaa gat gga tta tgg act tac ctc aat cag att gtg gcc tgt    1651
           Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln Ile Val Ala Cys
                            505                 510                 515

           tcc cct tgg gtt tta tat atc ttg atg cta gca act ttc cat ttc tca    1699
           Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr Phe His Phe Ser
                       520                 525                 530

           tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg    1747
           Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu
                535                 540                 545

           ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat    1795
           Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His
                550                 555                 560

           atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc    1843
           Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr Asn Leu Gly Phe
           565                 570                 575                 580

           atg cag aac ctg gca gat ttc ttt cag tgt ggc tgc ttt ggc ttg gtg    1891
           Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys Phe Gly Leu Val
                       585                 590                 595

           aag ccc tgt gtg gta gat tgg aca tca cag tac acc atg gtc ttt cac    1939
           Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr Met Val Phe His
                       600                 605                 610

           cca gcc agg gag aag gtt ctt cgc tca gta tgaagaaag caacccaaaa       1989
           Pro Ala Arg Glu Lys Val Leu Arg Ser Val
                615                 620

           ctctcaatct gatttgtttt tgtttatgtc gatgccctgt agtttgaaag tgaagtaaag  2049

           atttagaatt cacctaagtc caaaggaaaa cacgtggttt ttaaagccat taggtaaaaa  2109

           aagttctcaa taaaggcatt acaatttttt aggtttagaa agatggactt ttctgataaa  2169
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89

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tcttggcaga catctaaaaa aaaaaccata ttttttcacaa gaaaatgcaa gttacttttt 2229

ttggaaataa tactcactga ttatggataa aatggaatat tttcagatac tatattggct 2289

gtttcaaaat agtactattc tttaaacttg taattttttgc taagttattt gtctttgttg 2349

tatctataaa tatgtaaaaa atatttaaat agatgtacct gttttgcttt cacacttaat 2409

aaaaaatttt tttttgt                                                 2426


<210> 55
<211> 257
<212> PRT
<213> Homo sapiens

<400> 55
Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
  1               5                  10                  15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
             20                  25                  30

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
         35                  40                  45

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
     50                  55                  60

Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu
 65                  70                  75                  80

Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly
             85                  90                  95

Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg
            100                 105                 110

Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly Ala Gly
            115                 120                 125

Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser Thr Gly
    130                 135                 140

Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser Leu Gln
145                 150                 155                 160

His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro Gly Gly
                165                 170                 175

Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu Ala Leu
            180                 185                 190

Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile Leu Ala
            195                 200                 205
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90

Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val Ala Tyr
    210   215   220

Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys Leu Leu
225   230   235   240

Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala Thr Asp
                245   250   255

Gly

<210> 56
<211> 1520
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (10)..(780)

<400> 56
tttcccaag atg gcg tcg aag ata ggt tcg aga cgg tgg atg ttg cag ctg   51
          Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu
            1   5   10

atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg ggc   99
Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly
 15   20   25   30

tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc cgg   147
Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg
                35   40   45

aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca gcc   195
Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala
            50   55   60

gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg ttc   243
Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe
         65   70   75

gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc tac   291
Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr
     80   85   90

atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg tac   339
Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr
 95   100   105   110

tcg cgc aca gtt gcc atc atc ggc ggc ttt ctt gtg ttg gcc agc ggt   387
Ser Arg Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly
                115   120   125

gct ggg gag ctg tac cgc cgg aaa cct cgc agc cgc tcc ctg cag tcc   435
Ala Gly Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser

91

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acc ggc cag gtg ttc ctg ggt atc tac ctc atc tgt gtg gcc tac tca   483
Thr Gly Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser
        145               150               155

ctg cag cac agc aag gag gac cgg ctg gcg tat ctg aac cat ctc cca   531
Leu Gln His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro
    160               165               170

gga ggg gag ctg atg atc cag ctg ttc ttc gtg ctg tat ggc atc ctg   579
Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu
175               180               185               190

gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc   627
Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile
                195               200               205

ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt   675
Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val
            210               215               220

gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag   723
Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys
        225               230               235

ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc   771
Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala
    240               245               250

act gat ggc tgagttttat ggcaagaggc tgagatgggc acagggagcc           820
Thr Asp Gly
255

actgagggtc accctgcctt cctccttgct ggcccagctg ctgtttattt atgctttttg 880

gtctgtttgt ttgatctttt gctttttttaa aattgtttttt tgcagttaag aggcagctca 940

tttgtccaaa tttctgggct cagcgcttgg gagggcagga gccctggcac taatgctgta 1000

caggtttttt tcctgttagg agagctgagg ccagctgccc actgagtctc ctgtccctga 1060

gaagggagta tggcagggct gggatgcggc tactgagagt gggagagtgg gagacagagg 1120

aaggaagatg gagattggaa gtgagcaaat gtgaaaaatt cctctttgaa cctggcagat 1180

gcagctaggc tctgcagtgc tgtttggaga ctgtgagagg gagtgtgtgt gttgacacat 1240

gtggatcagg cccaggaagg gcacaggggc tgagcactac agaagtcaca tgggttctca 1300

gggtatgcca ggggcagaaa cagtaccggc tctctgtcac tcaccttgag agtagagcag 1360

accctgttct gctctgggct gtgaaggggt ggagcaggca gtggccagct ttgcccttcc 1420

tgctgtctct gtttctagct ccatggttgg cctggtgggg gtggagttcc ctcccaaaca 1480

ccagaccaca cagtcctcca aaaataaaca ttttatatag                       1520
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92

<210> 57
<211> 107
<212> PRT
<213> Homo sapiens

<400> 57
Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp Ile Gln
  1   5   10   15

Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys Asp Lys
                 20   25   30

Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln Val Glu
              35   40   45

Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe
        50   55   60

Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile
 65   70   75   80

Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His
                 85   90   95

Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
             100   105

<210> 58
<211> 1496
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (9)..(329)

<400> 58
ctaccagg atg gct ctc ttc gct ggt ggc aaa ctg cgt gtg cat ctc gac   50
        Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp
          1   5   10

atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa   98
Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys
 15   20   25   30

gat aag ctg acg gag cta cag ctc cgc gcc cgc cag ttg ctt gat cag 146
Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln
              35   40   45

gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag 194
Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu
              50   55   60

cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg 242

93

```
            Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp
                    65              70              75

tcc att gct cag act gtc atc ctc atc ctc act ggc atc tgg cag atg   290
Ser Ile Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met
    80              85              90

cgt cac ctc aag agc ttc ttt gag gcc aag aag ctg gtg tagtgccctc   339
Arg His Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
 95              100             105

tttgtatgac ccttcctttt tacctcattt atttggtact ttccccacac agtcctttat 399

ccacctggat ttttagggaa aaaaaatgaa aaagaataag tcacattggt tccatggcca 459

caaaccattc agatcagcca cttgctgacc ctggttctta aggacacatg acattagtcc 519

aatctttcaa aatcttgtct tagggcttgt gaggaatcag aactaaccca ggactcagtc 579

ctgcttcttt tgcctcgagt gattttcctc tgttttttcac taaataagca aatgaaaact 639

ctctccatta ccttctgctt tctctttgtc cacttacgca gtaggtgact ggcatgtgcc 699

acagagcagg ccctgcctca ctgtctgctg gtcagttctg ggttcactta atggctttgt 759

gaatgtaaat aaggggcagg tcttggccct agaggattga gatgttttc tatatcttag 819

aactattttt ggataaatta tatattttcc ttcctagtag aagtgttact gcctgtaact 879

agctcaaaat accaatgcag tttctgcatt ctgggttttg ttttttcttttttttttttttt 939

tttttttgagt tttgctcttg tcgcccaggc tggagtgcaa tggcgtgatc tcagctcact 999

ggcaacatct gcctcccggg ttcaaatgat tctcctgcct cagtctcctg agtagctggg 1059

attacaggtg cccgccacca cgctcagcta attttttgtat ttttagtaga gatggggttt 1119

taccatgttg gccaggctgg tcttagactc ctgacctcag ttgatccacc tgcctcagcc 1179

tctgcattca gtttattcac atatttttgg taactcccat ggcagctcct aggatttcag 1239

cggtctgtgg gccagaaagc aggcaccagg gctgacctca aggccgtatc agagggccaa 1299

gcagagttct tttggatacc tgcttttcat cccacagggc cttagagtca gaggtaaggt 1359

agcaacagag ctagaatggg gcaatgcact cttaccctcc ttctcaactt ttatttaagc 1419

tgtgctaaat gttttcttca agggaaccag atttagttct ttacagaatt ttccagtgaa 1479

ataaaacatg ttgtaat                                                 1496
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<210> 59
<211> 272
<212> PRT
<213> Homo sapiens

94

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Met Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly
1               5                   10                  15

Pro Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp
            20                  25                  30

Val Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met
            35                  40                  45

Met Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly
        50                  55                  60

Ile Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln
65                  70                  75                  80

Gly Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr
            85                  90                  95

Glu Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr
            100                 105                 110

Thr Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys
            115                 120                 125

Val Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg
    130                 135                 140

Glu Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu
145                 150                 155                 160

His Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro
            165                 170                 175

Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val
            180                 185                 190

Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr
            195                 200                 205

Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu
    210                 215                 220

Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln
225                 230                 235                 240

Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu
            245                 250                 255

Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu
            260                 265                 270
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<210> 60
<211> 1916
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (117)..(932)

<400> 60
atggtaacgg ctcggaagcc taggaggctg ggccggaggg aggcggagga accggtgttc 60

gccgccgccg ctgcttcagc ttattccttg tggcctctgc gggtcctgcc tcagcc atg 119
                                                                                       Met
                                                                                       1

atg atc cac ggc ttc cag agc agc cac cgg gat ttc tgc ttc ggg ccc 167
Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly Pro
                 5   10   15

tgg aag ctg acg gcg tcc aag acc cac atc atg aag tcg gcg gat gtg 215
Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp Val
        20   25   30

gag aaa tta gcc gat gaa tta cat atg cca tct ctc cct gaa atg atg 263
Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met Met
       35   40   45

ttt gga gac aac gtt tta aga atc cag cat ggg tct ggc ttt gga att 311
Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly Ile
 50   55   60   65

gag ttc aat gct aca gat gcg tta aga tgt gta aac aac tac caa gga 359
Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln Gly
                 70   75   80

atg ctt aaa gtg gcc tgt gct gaa gag tgg caa gaa agc agg acg gag 407
Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr Glu
                85   90   95

ggt gaa cac tcc aaa gag gtt att aaa cca tat gat tgg acc tat aca 455
Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr Thr
             100   105   110

aca gat tat aag gga acc tta ctt gga gaa tct ctt aag tta aag gtt 503
Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys Val
   115   120   125

gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa 551
Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu
130   135   140   145

cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat 599
Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His
             150   155   160

gat cat gga gtt tca agc ctg agt gtg aag att aga gta atg cct tct 647
Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser
             165   170   175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt 695

96

```
_Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val Leu
        180                 185             190

atc aga atg aat gac acg aga ctt tac cat gag gct gac aag acc tac   743
Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr
    195             200             205

atg tta cga gaa tat acg tca cga gaa agc aaa att tct agt ttg atg   791
Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu Met
210             215             220                 225

cat gtt cca cct tcc ctc ttc acg gaa cct aat gaa ata tcc cag tat   839
His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr
            230             235             240

tta cca ata aag gaa gca gtt tgt gag aag cta ata ttt cca gaa aga   887
Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu Arg
            245             250             255

att gat cct aac cca gca gac tca caa aaa agt aca caa gtg gaa       932
Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu
        260             265             270

taaaatgtga tacaacatat actcactatg gaatctgact ggacaccttg gctatttgta 992

aggggttatt tttattatga gaattaattg ccttgtttat gtacagattt tctgtagcct 1052

taaaggaaaa aaaaataaag atcgttacag gcaggtttca ctcaactgct atttgtactg 1112

tctgtcttca cattcatatt ccagatttat attttctgga gttaaatttg gatgatttct 1172

aaattatcac aaagtgggac ctcagcagta gtgatgtgtg tgtctcatga gcagtgagca 1232

cagtctgcat tcatcatgaa acactatctt ctaccaggag gaggttaatg taaatcacca 1292

aatcccaatg ccttgtgact ttcataggat tcctgatcat gcatgttgat gtactggctc 1352

ttcactttgg gctttctgat gtttattcac acctttggag agttgcaact tgccacatac 1412

gaaattagtc tcatagtgta gtgaacttca accccaaaat tttaaaaatg tatttccccc 1472

cagttttaaa ttgcctttga aatttaaaaa aaaaaattta gacttagtac cagaaccaaa 1532

aatacctaga tttttggaga acttattaca tacatagaaa catgaatatg gtttaccwct 1592

gtgtgtgtgt gtgtgtgtgt gtgtatacag actttttttt ttaacttgtt gattcagatg 1652

tcttggtccc tgaatagtcc tagattactt attttgagaa ttgattgtta aaaattacag 1712

ggaattaaaa taattgcctt tttttttta gagggtaaga gatgggtaga agagtatgcc 1772

tctgaaaatt ttattagttt attcttgtgg agaataccaa gaaaatgtgt atttgcccat 1832

tgctaaatat gatatatgcc attttgtatt tatttgtccc aagtgtcttt ttttaagagg 1892

agaataaaca ataaggaatt actg                                        1916
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97

<210> 61
<211> 219
<212> PRT
<213> Homo sapiens

<400> 61
Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser
 1   5   10   15

Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp
                20   25   30

Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln
        35   40   45

Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys
    50   55   60

Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp
65   70   75   80

Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile
                85   90   95

Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly
            100   105   110

Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile
            115   120   125

Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu
        130   135   140

Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu
145   150   155   160

Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala
                165   170   175

Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile
            180   185   190

Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val
            195   200   205

Asp Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser
            210   215

<210> 62
<211> 1362
<212> DNA
<213> Homo sapiens

<220>

98

<400> 62
gttttctggt tttgctctag tgtttgggtt tcttcgcggc tgctcaag atg aac cga 57
                                                        Met Asn Arg
                                                         1

ctc ttc ggg aaa gcg aaa ccc aag gct ccg ccg ccc agc ctg act gac 105
Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp
     5   10   15

tgc att ggc acg gtg gac agt aga gca gaa tcc att gac aag aag att 153
Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile
 20   25   30   35

tct cga ttg gat gct gag cta gtg aag tat aag gat cag atc aag aag 201
Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys
             40   45   50

atg aga gag ggt cct gca aag aat atg gtc aag cag aaa gcc ttg cga 249
Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg
             55   60   65

gtt tta aag caa aag agg atg tat gag cag cag cgg gac aat ctt gcc 297
Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala
         70   75   80

caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg 345
Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu
     85   90   95

aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa 393
Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu
100   105   110   115

atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta 441
Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu
             120   125   130

caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa 489
Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu
             135   140   145

gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta 537
Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu
             150   155   160

gaa gca gag ttg gat gca cta ggt gat gag ctt ctg gct gat gaa gac 585
Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp
     165   170   175

agt tct tat ttg gat gag gca gca tct gca cct gca att cca gaa ggt 633
Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly
180   185   190   195

gtt ccc act gat aca aaa aac aag gat gga gtt ctg gtg gat gaa ttt 681

99

```
    Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe
                    200                 205                 210

gga ttg cca cag atc cct gct tca tagatttgca tcattcaagc atatcttgta 735
Gly Leu Pro Gln Ile Pro Ala Ser
                215

aaacaaacac atattatggg actaggaaat atttatcttt ccaaatttgc cataacagat 795

ttaggtttct ttcctttctt tgaaggaaag tttaattaca ttgctctttt attttttcca 855

ttaagagact cattgcttgg gaaatgcttt cttcgtacta aaatttgatt cctttttttt 915

cttatgaaaa acgaactcag tttaaaagta tttttagctc gtatgacttg ttttcattca 975

ttaataataa tttgaaataa aactaaggaa atggaatctt aaaagtctat gacagtgtaa 1035

ctctacagtc tcaaaatgac ctgataaatt gataagacaa agatgagatt attggggctg 1095

ttcatattat gattcagaat cattttctat tgtggtatta taggttggtt aaagtgatgg 1155

ccttttttgat gggtttttgtt gtgtcttgtg aacaagtcgt tactgtgtcc attattggaa 1215

tggaattatc actactgtat catgagtggg tattttgatt ctatggttcc ctcagtatta 1275

catcttgact tgtaatcaat tatgaatatt tcttgatatt taatgtatag gacatttatt 1335

tatactcaat aaatattttt caaaagg                                      1362


<210> 63
<211> 622
<212> PRT
<213> Homo sapiens

<400> 63
Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro
  1               5                  10                  15

Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His Tyr Asn His Gly
                20                  25                  30

Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp Asp Tyr Ser Thr
            35                  40                  45

Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg
    50                  55                  60

Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn
 65                  70                  75                  80

Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg Ile Asp Leu Val
                85                  90                  95

Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln Leu Gly Gly Asp
                100                 105                 110
```

100

Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln Gly His Leu Ser
    115   120   125

Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp
    130   135   140

Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln Phe Gly His Thr
145   150   155   160

Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp Val Asp Met Met
                165   170   175

Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala Tyr Arg Thr His
            180   185   190

Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn Val Ser Val Asn
            195   200   205

Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His Trp Ala Val Leu
    210   215   220

Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn
225   230   235   240

Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys
            245   250   255

Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln Glu Ala Arg Gln
        260   265   270

Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp
    275   280   285

Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro Phe Leu Val Ile
    290   295   300

Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile
305   310   315   320

Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val Gln Phe Leu Ser
            325   330   335

Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu Pro Leu Gly Ile
            340   345   350

Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp Phe Phe Trp Phe
            355   360   365

Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro Phe Leu Ala Asn
    370   375   380

Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro
385   390   395   400

Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys Thr Ile Val Glu
            405   410   415

101

```
Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys
        420                 425                 430

Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg
        435                 440                 445

Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
    450                 455                 460

Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu
465                 470                 475                 480

Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu
                485                 490                 495

His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr
            500                 505                 510

Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser
        515                 520                 525

Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr
    530                 535                 540

Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg
545                 550                 555                 560

Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile Glu Ser Pro Phe
                565                 570                 575

Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys
                580                 585                 590

Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr Arg Gln Tyr Thr
        595                 600                 605

Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val
610                 615                 620


<210> 64
<211> 2948
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (14)..(1879)

<400> 64
atttaacacc aag atg gcg gac ggc ccg gat gag tac gat acc gaa gcg      49
            Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala
              1               5                  10

ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat     97
Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His
        15                  20                  25
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102

```
tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat    145
Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp
        30                  35                  40

gat tac agc aca tgg gac ata gtc aag gct aca caa tat gga ata tat    193
Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr
45                  50                  55                  60

gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta cgg caa ccg    241
Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro
                65                  70                  75

gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc aat aac aga    289
Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg
                80                  85                  90

ata gat tta gtc aaa tac tat att tcg aaa ggt gct att gtg gat caa    337
Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln
            95                  100                 105

ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc aca aga caa    385
Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln
    110                 115                 120

ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt gca gat cct    433
Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro
125                 130                 135                 140

tca tta att gat gga gaa gga tgt agc tgt att cat ctg gct gct cag    481
Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln
                145                 150                 155

ttc gga cat acc tca att gtt gct tat ctc ata gca aaa gga cag gat    529
Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp
            160                 165                 170

gta gat atg atg gat cag aat gga atg acg cct tta atg tgg gca gca    577
Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala
        175                 180                 185

tat aga aca cat agt gtg gat cca act aga ttg ctt tta aca ttc aat    625
Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn
    190                 195                 200

gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act gct ctg cat    673
Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His
205                 210                 215                 220

tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt ctt ctg gaa    721
Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu
                225                 230                 235

gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa tca gcg ctt    769
Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu
            240                 245                 250
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103

```
- gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac cac tta caa  817
  Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln
          255                 260                 265

  gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc ctt aga aag  865
  Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys
          270                 275                 280

  ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta gga act cct  913
  Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro
  285                 290                 295                 300

  ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta aat att gat  961
  Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp
                  305                 310                 315

  tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg gct aca gta  1009
  Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val
                  320                 325                 330

  cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat agt gca ttg  1057
  Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu
          335                 340                 345

  ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg  1105
  Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp
          350                 355                 360

  ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc cat ctt cca  1153
  Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro
  365                 370                 375                 380

  ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga aaa tct tgg  1201
  Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp
                  385                 390                 395

  aaa tca gat cca ggg att att aaa gca aca gaa gag caa aag aaa aag  1249
  Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys
                  400                 405                 410

  aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc agt ata ttc  1297
  Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe
          415                 420                 425

  tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa cat tgt ggt  1345
  Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly
          430                 435                 440

  gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc cca tgg gtg  1393
  Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val
  445                 450                 455                 460

  ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg ggc tac cta  1441
  Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu
                  465                 470                 475

  ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt tgt ata tct  1489
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104

```
     Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser
                 480                 485                 490

tac tgg gga ctc cac tgt gag acc act tac acc aag gat gga ttt tgg   1537
Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp
        495                 500                 505

aca tac att act cag att gcc acg tgt tca cct tgg atg ttt tgg atg   1585
Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met
        510                 515                 520

ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta tta ctc atg   1633
Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val Leu Leu Met
525                 530                 535                 540

tgt cag atg tac cag ata tca tgt tta ggt att act aca aat gaa aga   1681
Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg
                545                 550                 555

atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca acg tct att   1729
Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile
                560                 565                 570

gaa agc cca ttc aac cat gga tgt gta aga aat att ata gac ttc ttt   1777
Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe
        575                 580                 585

gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg gac tgg acc   1825
Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr
        590                 595                 600

agg cag tat aca ata gaa tat gac caa ata tca gga tct ggg tac cag   1873
Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln
605                 610                 615                 620

ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtggtg cctgaaaatt   1929
Leu Val

gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga gcatgctatg 1989

tgtagggcta atggtgaatt ttacagtctt tttttcaaca cttttattaa caaaagtaaa 2049

catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa taattttaat 2109

ggttcttaat gtggaaattc acaacatact caacttttgg gttttgttct cacagtattt 2169

ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat cagaaatgtt 2229

cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc agtctagtac 2289

gagtattgca tctaattcca ggagcattgt tttaagttga ttgactagtt attatgtaca 2349

tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc tactgtgatg 2409

ttgtcttcaa aggcaggaga aaataatgtt cacaataaaa tgtgctaaca atgttttgtt 2469

tctatcagct gttgcaatgc tgatatattt ctagttcagt gaaataattt gtagtaacct 2529
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105

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tactctgagg  ttttacggtc  tgataatgaa  gcacttgcat  gagtatagta  agtcatgttt  2589

ttttgttcaa  atttaaaagc  cctgctaatt  gcatgacaca  ccacatagaa  tgtatactag  2649

cagatactat  ccagtgaagc  ataaattaga  atttaatttg  atgttcaaaa  acagttccat  2709

ttttaagggt  taaggtggta  ttttcaagaa  aaggcagaac  aaataatgca  aaattctcag  2769

taatagtgat  acatggatat  acttcctttt  aaattctcag  ctgcaaaata  attgtagaca  2829

aaataatggc  atttaactaa  agatggagca  tgatctgtgt  acatagcaca  tgtgaataaa  2889

agaaaagctg  acagtatatt  ctggtttcaa  taaaatgacc  tatcagaaag  tagaatttc  2948
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<210> 65
<211> 632
<212> PRT
<213> Homo sapiens

<400> 65

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Met Gln Arg Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp
 1               5                   10                  15

Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu
            20                  25                  30

Ile Lys Pro Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly
        35                  40                  45

Arg Lys Thr His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala
    50                  55                  60

Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly
65                  70                  75                  80

Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp
                85                  90                  95

Ala Ala Ile Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys
            100                 105                 110

Gly Ala Ile Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu
            115                 120                 125

His Trp Ala Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met
    130                 135                 140

Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys
145                 150                 155                 160

Ile His Leu Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu
                165                 170                 175

Ile Ala Lys Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr
            180                 185                 190
```

106

```
Pro Leu Met Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg
    195             200             205

Leu Leu Leu Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His
    210             215             220

Lys Asn Thr Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val
225             230             235             240

Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile
            245             250             255

Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp
            260             265             270

Met Ile Asn His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn
    275             280             285

Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys
    290             295             300

Val Met Leu Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile
305             310             315             320

Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly
            325             330             335

Gly Val Trp Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His
            340             345             350

Ser Met His Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe
            355             360             365

Trp Met Tyr Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe
    370             375             380

Leu Phe Ile His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr
385             390             395             400

Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr
            405             410             415

Glu Glu Gln Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser
            420             425             430

Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val
    435             440             445

Arg Ser Lys His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp
    450             455             460

His His Cys Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg
465             470             475             480

Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met
            485             490             495
```

107

```
Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr
            500                 505                 510

Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser
            515                 520                 525

Pro Trp Met Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp
            530                 535                 540

Val Ala Val Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly
545                 550                 555                 560

Ile Thr Thr Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys
                565                 570                 575

Val Thr Thr Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg
                580                 585                 590

Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro
                595                 600                 605

Val Ile Val Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile
            610                 615                 620

Ser Gly Ser Gly Tyr Gln Leu Val
625                 630


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cctccgcctc gcccgagccc cgggagggtg aaacgctttc tcccagc atg cag cgg    116
                                                     Met Gln Arg
                                                      1

gag gag gga ttt aac acc aag atg gcg gac ggc ccg gat gag tac gat    164
Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp Glu Tyr Asp
      5                 10                  15

acc gaa gcg ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc    212
Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro
 20                 25                  30                  35

caa agc cat tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act    260
Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr
                40                  45                  50
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108

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-cat -att gat gat-tac agc aca tgg-gac ata gtc aag-gct aca caa tat      308-
 His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr
             55                  60                  65

 gga ata tat gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta      356
 Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val
             70                  75                  80

 cgg caa ccg gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc      404
 Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile
             85                  90                  95

 aat aac aga ata gat tta gtc aaa tac tat att tcg aaa ggt gct att      452
 Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile
 100                 105                 110                 115

 gtg gat caa ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc      500
 Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala
                 120                 125                 130

 aca aga caa ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt      548
 Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly
                 135                 140                 145

 gca gat cct tca tta att gat gga gaa gga tgt agc tgt att cat ctg      596
 Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu
                 150                 155                 160

 gct gct cag ttc gga cat acc tca att gtt gct tat ctc ata gca aaa      644
 Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys
                 165                 170                 175

 gga cag gat gta gat atg atg gat cag aat gga atg acg cct tta atg      692
 Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met
 180                 185                 190                 195

 tgg gca gca tat aga aca cat agt gtg gat cca act aga ttg ctt tta      740
 Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu
                 200                 205                 210

 aca ttc aat gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act      788
 Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr
                 215                 220                 225

 gct ctg cat tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt      836
 Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu
                 230                 235                 240

 ctt ctg gaa gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa      884
 Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu
                 245                 250                 255

 tca gcg ctt gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac      932
 Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn
 260                 265                 270                 275

 cac tta caa gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc      980
```

109

His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe
                    280   285   290

ctt aga aag ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta   1028
Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu
            295   300   305

gga act cct ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta   1076
Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu
            310   315   320

aat att gat tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg   1124
Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp
    325   330   335

gct aca gta cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat   1172
Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His
340   345   350   355

agt gca ttg ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat   1220
Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr
                360   365   370

gtg acg tgg ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc   1268
Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile
                375   380   385

cat ctt cca ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga   1316
His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly
            390   395   400

aaa tct tgg aaa tca gat cca ggg att att aaa gca aca gaa gag caa   1364
Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln
            405   410   415

aag aaa aag aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc   1412
Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu
420   425   430   435

agt ata ttc tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa   1460
Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys
                440   445   450

cat tgt ggt gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc   1508
His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys
                455   460   465

cca tgg gtg ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg   1556
Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met
            470   475   480

ggc tac cta ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt   1604
Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly
    485   490   495

tgt ata tct tac tgg gga ctc cac tgt gag acc act tac acc aag gat   1652
Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp

110

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gga ttt tgg aca tac att act cag att gcc acg tgt tca cct tgg atg   1700
Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met
            520                 525                 530

ttt tgg atg ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta   1748
Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val
            535                 540                 545

tta ctc atg tgt cag atg tac cag ata tca tgt tta ggt att act aca   1796
Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr
            550                 555                 560

aat gaa aga atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca   1844
Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr
            565                 570                 575

acg tct att gaa agc cca ttc aac cat gga tgt gta aga aat att ata   1892
Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile
580                 585                 590                 595

gac ttc ttt gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg   1940
Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val
                600                 605                 610

gac tgg acc agg cag tat aca ata gaa tat gac caa ata tca gga tct   1988
Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser
            615                 620                 625

ggg tac cag ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtggtg   2043
Gly Tyr Gln Leu Val
            630

cctgaaaatt gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga 2103

gcatgctatg tgtagggcta atggtgaatt ttacagtctt tttttcaaca cttttattaa 2163

caaaagtaaa catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa 2223

taattttaat ggttcttaat gtggaaattc acaacatact caacttttgg gtttttgttct 2283

cacagtattt ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat 2343

cagaaatgtt cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc 2403

agtctagtac gagtattgca tctaattcca ggagcattgt tttaagttga ttgactagtt 2463

attatgtaca tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc 2523

tactgtgatg ttgtcttcaa aggcaggaga aaataatgtt cacaataaaa tgtgctaaca 2583

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111

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tgtatactag cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa 2823

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aaattctcag taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata 2943

attgtagaca aaataatggc atttaactaa agatggagca tgatctaagt acatagcaca 3003

tgtgaataaa agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag 3063

tagaatttca tccccaagag tatttcagtt tatccaatat tgagtaagtt ctgaaacagt 3123

tttagaaaaa attttctttt tgttaaatgt gatgcactga tcaatttttg tcacagcatt 3183

ttcatacctt catggtggac tactagtcac tgcttccata aatattgttt acagggtgag 3243

atttggttta ttcatcttaa gtgctgtagc aaactgtggt tcgagcaacc tgtgggaaat 3303

ctgtgagagg gaatggggtg ggagatgtgg gggaatggtg gtcagactga tgacagatcc 3363

tagaccaatg taaagaatgt gtatctgtat ataaataatt tatcaaatag ttttctcttt 3423

gtgtctgtgt tagtgttttt aaagctgctc atttcatttt gtccaaccaa aaagaaaagg 3483

gagataacta atgagcttct agtgatgttc aaaattgctg ttaataggca ttataccctg 3543

caagttcact gcatgtctga tgcttggtaa aactagtctt ccctgtaaaa tgcagattac 3603

aggtattaaa gcaatctagt ggtatacccg ccccttgcct tagtaagagg agcagtgaaa 3663

tgtatatagt tgatgttcag tatttccaag taccattttt atatagtagc ttatttgacc 3723

ataagtcaca catcaaaaaa agattaccct tagtgtatgt gttttaatat tagaaaattg 3783

gcatatgtac tttatttttg aaaagggaag agatgggtgt ggggtggcaa tagcattgtg 3843

ccattttgtc atagaatgta aaaattggtt aactttacaa atgtcagcta gttttgacta 3903

ctaattgggg gaaattttag ataattttta aattcaaagt tatttataaa atgctagaat 3963

ttgttttaat tttttgtatt ttgagccact tcacatgaag actcagttgc atttttatcg 4023

aatacatttt tatcaacagt taaagactat ggtggttttt tcagagtttg gctaagaatg 4083

ttgttaccat cttctttgtt tgtggtacaa tattttcagt gcaaagagaa tgtcattcag 4143

ttaaaaagac aaacctctag atgtgtaatt acatggaaaa tactagcaat gtgaatgctt 4203

ttgtagtaac catcttgtag tacctgtgaa atctataact cagaaatggt cagatggtca 4263

ggagccagct atgcagcagt ataccatctg tttaattatt ttgtaggtcc tgtgtgtgga 4323

accaactata aacccagttc taaagttgtg tatgatggtg aacctttggg aatagttctt 4383

atcaacttaa ttggatactt ttagcaaata ggaacttaat tctcagcact gaacatgaat 4443
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112

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tttatttata actgtgccaa gtattatttt gctacttacc gtgttattct gtggaaagaa 4623

aaacctgtaa agtgtttaat aaattagccc tccttacata aattaaatgt caaaattttg 4683

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Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp
             20                  25                  30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu
          35                  40                  45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly
       50                  55                  60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr
 65                  70                  75                  80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr
                85                  90                  95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
             100                 105                 110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
         115                 120                 125

Val Gln Trp Gln Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
     130                 135                 140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
145                 150                 155                 160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
             165                 170                 175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
             180                 185                 190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
         195                 200                 205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn
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113

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
225   230   235   240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
              245   250   255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
              260   265   270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
              275   280   285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
              290   295   300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
305   310   315   320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
              325   330   335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
              340   345   350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
              355   360   365

Met His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
              370   375   380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
385   390   395   400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
              405   410   415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
              420   425   430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
              435   440   445

Gly Gln Met Arg Pro Glu Gly Val Gly Leu Pro Ala Glu Val Thr Gln
              450   455   460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
465   470   475   480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
              485   490   495

Ser Cys

114

<210> 68
<211> 1902
<212> DNA
<213> Homo sapiens

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<222> (22)..(1515)

<400> 68
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                         Met Ala Arg Leu Glu Val Ile Glu Leu Pro
                         1               5                   10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac     99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His
                15                  20                  25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att    147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile
            30                  35                  40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg    195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val
        45                  50                  55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc    243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly
    60                  65                  70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa    291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu
75                  80                  85                  90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct    339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro
                95                  100                 105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg    387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg
            110                 115                 120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag    435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu
            125                 130                 135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc    483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly
        140                 145                 150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac    531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn
155                 160                 165                 170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag    579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln
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115

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gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg   627
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val
        190             195             200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg   675
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val
        205             210             215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct   723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro
    220             225             230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg   771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu
235             240             245             250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc   819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala
                255             260             265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag   867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys
            270             275             280

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac   915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp
        285             290             295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca   963
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro
    300             305             310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc   1011
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu
315             320             325             330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc   1059
Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly
            335             340             345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg   1107
Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr
            350             355             360

cac acc ctg aac agc acg atg cac gag tac aag atc caa ggc ctc tca   1155
His Thr Leu Asn Ser Thr Met His Glu Tyr Lys Ile Gln Gly Leu Ser
        365             370             375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc   1203
Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly
    380             385             390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac   1251
Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp
395             400             405             410
```

116

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ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc   1299
Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg
                415                 420                 425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc   1347
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile
                430                 435                 440

tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta   1395
Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu
            445                 450                 455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca   1443
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala
        460                 465                 470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc   1491
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser
475                 480                 485                 490

cag aaa ctt tgg gaa ttc tct tgt tagttggtta gttttactgt aattttctat   1545
Gln Lys Leu Trp Glu Phe Ser Cys
                495

aaagaattca tatcatctgt taatggcgac agtttttgtt tcttcctttg aatttttttat  1605

attctttctt tctcttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg   1665

gctaaagcgt cttctatcat atcgaattgg acaatgata gaagacaatc tttgttttgt   1725

cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt   1785

aggctttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgatcctg   1845

atttcctagg agttggtttt tttttttta aagcataaat aaatttaatt gcatcag     1902


<210> 69
<211> 498
<212> PRT
<213> Homo sapiens

<400> 69
Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu
  1               5                  10                  15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp
                20                  25                  30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu
            35                  40                  45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly
        50                  55                  60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr
```

117

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr
                85   90   95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
               100   105   110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
               115   120   125

Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
           130   135   140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
145   150   155   160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
               165   170   175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
           180   185   190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
           195   200   205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn
           210   215   220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
225   230   235   240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
               245   250   255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
           260   265   270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
           275   280   285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
           290   295   300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
305   310   315   320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
               325   330   335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
               340   345   350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
           355   360   365

Thr His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr

118

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
385   390   395   400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
                405   410   415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
                420   425   430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
            435   440   445

Gly Gln Met Arg His Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln
    450   455   460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
465   470   475   480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
                485   490   495

Ser Cys

<210> 70
<211> 1902
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (22)..(1515)

<400> 70
gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct   51
                        Met Ala Arg Leu Glu Val Ile Glu Leu Pro
                         1   5   10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac   99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His
                15   20   25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att   147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile
             30   35   40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg   195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val
             45   50   55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc   243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly
    60   65   70

```
ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa    291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu
 75                  80                  85                  90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct    339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro
                 95                 100                 105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg    387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg
                110                 115                 120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag    435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu
                125                 130                 135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc    483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly
                140                 145                 150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac    531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn
155                 160                 165                 170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag    579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln
                175                 180                 185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg    627
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val
                190                 195                 200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg    675
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val
                205                 210                 215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct    723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro
                220                 225                 230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg    771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu
235                 240                 245                 250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc    819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala
                255                 260                 265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag    867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys
                270                 275                 280

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac    915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp
                285                 290                 295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca    963
```

120

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc   1011
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu
315   320   325   330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc   1059
Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly
                335   340   345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg   1107
Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr
                350   355   360

cac acc ctg aac agc acg acg cac gag tac aag atc caa ggc ctc tca   1155
His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly Leu Ser
                365   370   375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc   1203
Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly
    380   385   390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac   1251
Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp
395   400   405   410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc   1299
Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg
                415   420   425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc   1347
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile
                430   435   440

tcc agg tgg att gtt gag ggg cag atg aga cat caa ggt gtt gga tta   1395
Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val Gly Leu
                445   450   455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca   1443
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala
    460   465   470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc   1491
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser
475   480   485   490

cag aaa ctt tgg gaa ttc tct tgt tagttggtta gttttactgt aattttctat   1545
Gln Lys Leu Trp Glu Phe Ser Cys
                495

aaagaattca tatcatctgt taatggcgac agtttttgtt cttcctttg aatttttttat   1605

attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg   1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgtttttgt   1725

121

cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt 1785

aggctttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgatcctg 1845

atttcctagg agttggtttt ttttttttta aagcataaat aaatttaatt gcatcag   1902

<210> 71
<211> 245
<212> PRT
<213> Homo sapiens

<400> 71
Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His
 1   5   10   15

Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr
            20   25   30

Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr
        35   40   45

Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro
    50   55   60

Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly
65   70   75   80

Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro
                85   90   95

Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp
            100   105   110

Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr
        115   120   125

Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala
    130   135   140

Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu
145   150   155   160

Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys
                165   170   175

Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly
            180   185   190

Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val
        195   200   205

Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg
    210   215   220

Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val Leu Gly
225   230   235   240

122

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Gln Trp Ile Gln Arg
                245


<210> 72
<211> 1551
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (127)..(861)

<400> 72
ggaagtcggc caccttcctc cgtcccggcc gttagcccag ccaagcccag ccaagcccag 60

ccaagccccg ccgatcgcgg gcaccggagc cagccccgca gcgggtcccg cctgtctgtc 120

acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct     168
       Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser
        1               5                   10

atg cac tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc   216
Met His Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser
 15                  20                  25                  30

atg acc aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc   264
Met Thr Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile
                 35                  40                  45

ctg acg ttc ttt gtg ggt gct gcc atc ctc tgg ctg ctc tgc tcc cac   312
Leu Thr Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His
                 50                  55                  60

cgc ccg gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg   360
Arg Pro Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg
             65                  70                  75

ctc ggc cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct   408
Leu Gly Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser
     80                  85                  90

ccc cca caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc   456
Pro Pro Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile
 95                  100                 105                 110

gca gac ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc   504
Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe
                 115                 120                 125

agt tac ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag   552
Ser Tyr Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys
             130                 135                 140

gtg gcc gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg   600
Val Ala Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu
```

123

```
gcg gag aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat   648
Ala Glu Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn
    160                     165             170

ggg aaa ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc   696
Gly Lys Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile
175             180                 185                 190

gaa ggc agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc   744
Glu Gly Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly
                195                 200                 205

acc gtg gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg cgg gag att   792
Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile
            210                 215                 220

gta agg aag cgg tgg cgg ctg gtg aag caa gtc tca cat gtc ggc gtt   840
Val Arg Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val
        225                 230                 235

ctt ggc caa tgg ata caa aga taaagaaaat gttgcctttt tctaggaact       891
Leu Gly Gln Trp Ile Gln Arg
    240                 245

gtcagaaatc ctcatgcctt tcaagacttc tgtgaatgac ttgaattttt tattccctgc 951

ctagggtctg tgaacgaggc ctgtctcttc cctggggttt ctttccatgg cctttatttc 1011

tcctcttcca gtgggagttt tgcaggctct tctctgtgga aacttcacga gcgttggctg 1071

ggcctcggct tcgctggagt gtactccagg gtgaaggcag agtgggattt gagacccagg 1131

tagtggagga agcgaaggaa gtgaacgctg aatgtgacgc atttctgaag agctcagctg 1191

tcaccgggca tagcctggaa gccccaagtc tgttctgact ttgcctggct gtctccttga 1251

cccgcctcct agatcattgt ccttgatgtc caggctgggt catttaaaat agagatgcaa 1311

tcaggaaggt tgggggactt gggactgtgg ctgaattgag accttgctga tgtattcatg 1371

tcagcacctg agtcacagcc caggtgcccg gaagcagcct cttcgcatag gcagtgattt 1431

gcgattactt taaagctcac cttttttctt cccctctctg ttcgctgctg tcagcataat 1491

gattgtgttc cttccctatg ggatccatct gttttgtaaa caataaagcg tctgagggag 1551
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<210> 73
<211> 352
<212> PRT
<213> Homo sapiens

<400> 73
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Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
  1               5                  10                  15
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124

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Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
        20              25              30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
        35              40              45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
    50              55              60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
65              70              75              80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
        85              90              95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
        100             105             110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
        115             120             125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
    130             135             140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
145             150             155             160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
        165             170             175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
        180             185             190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
        195             200             205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
    210             215             220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
225             230             235             240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
        245             250             255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
        260             265             270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
        275             280             285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
    290             295             300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305             310             315             320
```

125

```
Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
                325                 330                 335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser
                340                 345                 350


<210> 74
<211> 2401
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (103)..(1158)

<400> 74
ttaggccggg ggggtgcggt cctggtcgga aggaggtgga gagtcggggg tcaccaggcc   60

tatccttggc gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga     114
                                                  Met Glu Ser Gly
                                                    1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg   162
Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
  5                  10                  15                  20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc   210
Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
                25                  30                  35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag   258
Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys
                40                  45                  50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata   306
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
                55                  60                  65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg   354
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
      70                  75                  80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag   402
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
 85                  90                  95                 100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc   450
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
                105                 110                 115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag   498
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu
                120                 125                 130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg   546
```

126

```
    Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val
            135                 140                 145


    gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag    594
    Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln
        150                 155                 160


    tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa    642
    Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys
    165                 170                 175                 180


    ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca    690
    Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr
                    185                 190                 195


    ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg    738
    Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro
                200                 205                 210


    ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc    786
    Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser
                215                 220                 225


    ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg    834
    Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala
                230                 235                 240


    ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg    882
    Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg
    245                 250                 255                 260


    aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag    930
    Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln
                    265                 270                 275


    gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct    978
    Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro
                    280                 285                 290


    gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc    1026
    Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser
                295                 300                 305


    ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc    1074
    Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr
        310                 315                 320


    gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga    1122
    Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg
    325                 330                 335                 340


    cag gcg atc acc cgg gtg ata ccc ccg tac aac agc taatagtttg    1168
    Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser
                    345                 350


    gaagccgcac agcttgacct ggaagcaccc ctgccccctt ttcagggatt tttatctcga 1228
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127

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  ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

  tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348

  gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg 1408

  tctcctccca ggagccagat cagtgcgagt gtgactgaaa atgcctcatc acttaagcac 1468

  caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgttttttc tggtgaatcg 1528

  ttgcttgctg tggacttggt ggaggactca gaggggagga aaggctgggc cccgagtaca 1588

  acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt cttttttcctc 1648

  atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcaggtcaa cttgtgttcc 1708

  tttcccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag 1768

  tgaagtcagc acatccgctt ctgcccagat ggtcggggcc ccgggcaaca gattgaagag 1828

  agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttcgccactg gccctgattt 1888

  gaactcctgc cacttgggag agctcggggt ggtccctggt tttccctcct ggagaatgag 1948

  gcgcagaggc ctcgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

  ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068

  tgccctcttg gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128

  tcgcttctcc ttgtgttacc ccctcccagt attaccattt gcccctcacc tgcccttggt 2188

  gagccttta gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc 2248

  acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcatc tctcgtcctc 2308

  ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

  gtgtgaacag cagaaattaa acatgttgca acc                              2401


<210> 75
<211> 352
<212> PRT
<213> Homo sapiens

<400> 75
Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
 1               5                  10                  15

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
            20                  25                  30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
        35                  40                  45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
```

128

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
65   70   75   80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
            85   90   95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
            100   105   110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
            115   120   125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
    130   135   140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
145   150   155   160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
            165   170   175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
            180   185   190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
    195   200   205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
210   215   220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
225   230   235   240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
            245   250   255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
            260   265   270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
            275   280   285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
    290   295   300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305   310   315   320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
            325   330   335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
            340   345   350

<210> 7.6
<211> 2401
<212> DNA
<213> Homo sapiens

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<400> 76
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tatccttggc gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga   114
                                                Met Glu Ser Gly
                                                 1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg   162
Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
 5   10   15   20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc   210
Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
                25   30   35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag   258
Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys
                40   45   50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata   306
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
            55   60   65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg   354
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
        70   75   80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag   402
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
 85   90   95   100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc   450
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
                105   110   115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag   498
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu
                120   125   130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg   546
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val
            135   140   145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag   594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln
    150   155   160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa   642

```
Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys
165             170             175             180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca    690
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr
                185             190             195

ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg    738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro
                200             205             210

ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc    786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser
                215             220             225

ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg    834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala
    230             235             240

ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg    882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg
245             250             255             260

aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag    930
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln
                265             270             275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct    978
Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro
                280             285             290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc   1026
Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser
                295             300             305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc   1074
Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr
    310             315             320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga   1122
Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg
325             330             335             340

cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagtttg        1168
Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
                345             350

gaagccgcac agcttgacct ggaagcaccc ctgccccctt ttcagggatt tttatctcga 1228

ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348

gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg 1408

tctcctccca ggagccagat cagtgcgagt gtgactgaaa atgcctcatc acttaagcac 1468
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131

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caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgtttttttc tggtgaatcg 1528

ttgcttgctg tggacttggt ggaggactca gaggggagga aaggctgggc cccgagtaca 1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt cttttttcctc 1648

atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcaggtcaa cttgtgttcc 1708

tttcccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag 1768

tgaagtcagc acatccgctt ctgcccagat ggtcggggcc ccgggcaaca gattgaagag 1828

agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttcgccactg gccctgattt 1888

gaactcctgc cacttgggag agctcggggt ggtccctggt tttccctcct ggagaatgag 1948

gcgcagaggc ctcgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068

tgccctcttg gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128

tcgcttctcc ttgtgttacc ccctcccagt attaccattt gcccctcacc tgcccttggt 2188

gagcctttta gtgcaagaca gatgggggctg ttttccccca cctctgagta gttggaggtc 2248

acatacacag ctctttttt attgcccttt tctgcctctg aatgttcatc tctcgtcctc 2308

ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc                               2401


<210> 77
<211> 697
<212> PRT
<213> Homo sapiens

<400> 77
Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu Tyr Leu Ala
1               5                   10                  15

Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met His Ser Ser
            20                  25                  30

Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu Val Ala Ile
        35                  40                  45

Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn Ser Leu Ile
    50                  55                  60

Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile Ala Ser Ile
65                  70                  75                  80

Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser Leu Ser Asn
                85                  90                  95
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132

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Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser
        100             105             110

Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu
        115             120             125

Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg Ile Ser
    130             135             140

Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu Phe Leu
145             150             155             160

Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val Glu Lys
            165             170             175

Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu Ile Ile
        180             185             190

Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val Ile Phe
        195             200             205

Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile
    210             215             220

Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp
225             230             235             240

Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu
            245             250             255

Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met
            260             265             270

Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr
        275             280             285

His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe
    290             295             300

Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His
305             310             315             320

Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp
            325             330             335

Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe
            340             345             350

Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala
        355             360             365

Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser
    370             375             380

Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe
385             390             395             400
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133

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            His  Glu  Leu  Gly  Asn  Cys  Leu  Gly  Gly  Thr  Ser  Val  Gly  Tyr  Ala  Ile
                             405                      410                      415

       Val  Ile  Pro  Thr  Asn  Phe  Cys  Ser  Pro  Asp  Gly  Gln  Pro  Thr  Leu  Leu
                      420                      425                      430

       Pro  Pro  Glu  His  Val  Gln  Glu  Leu  Asn  Leu  Arg  Ser  Thr  Gly  Met  Leu
                      435                      440                      445

       Asn  Ala  Ile  Gln  Arg  Phe  Phe  Ala  Tyr  His  Met  Ile  Glu  Thr  Tyr  Gly
            450                      455                      460

       Cys  Asp  Tyr  Ser  Thr  Ser  Gly  Leu  Ser  Phe  Asp  Thr  Leu  His  Ser  Lys
       465                      470                      475                      480

       Leu  Lys  Ala  Phe  Leu  Glu  Leu  Arg  Thr  Val  Asp  Gly  Pro  Arg  His  Asp
                      485                      490                      495

       Thr  Tyr  Ile  Leu  Tyr  Tyr  Ser  Gly  His  Thr  His  Gly  Thr  Gly  Glu  Trp
                      500                      505                      510

       Ala  Leu  Ala  Gly  Gly  Asp  Thr  Leu  Arg  Leu  Asp  Thr  Leu  Ile  Glu  Trp
                      515                      520                      525

       Trp  Arg  Glu  Lys  Asn  Gly  Ser  Phe  Cys  Ser  Arg  Leu  Ile  Ile  Val  Leu
                      530                      535                      540

       Asp  Ser  Glu  Asn  Ser  Thr  Pro  Trp  Val  Lys  Glu  Val  Arg  Lys  Ile  Asn
       545                      550                      555                      560

       Asp  Gln  Tyr  Ile  Ala  Val  Gln  Gly  Ala  Glu  Leu  Ile  Lys  Thr  Val  Asp
                      565                      570                      575

       Ile  Glu  Glu  Ala  Asp  Pro  Pro  Gln  Leu  Gly  Asp  Phe  Thr  Lys  Asp  Trp
                      580                      585                      590

       Val  Glu  Tyr  Asn  Cys  Asn  Ser  Ser  Asn  Asn  Ile  Cys  Trp  Thr  Glu  Lys
                      595                      600                      605

       Gly  Arg  Thr  Val  Lys  Ala  Val  Tyr  Gly  Val  Ser  Lys  Arg  Trp  Ser  Asp
            610                      615                      620

       Tyr  Thr  Leu  His  Leu  Pro  Thr  Gly  Ser  Asp  Val  Ala  Lys  His  Trp  Met
       625                      630                      635                      640

       Leu  His  Phe  Pro  Arg  Ile  Thr  Tyr  Pro  Leu  Val  His  Leu  Ala  Asn  Trp
                      645                      650                      655

       Leu  Cys  Gly  Leu  Asn  Leu  Phe  Trp  Ile  Cys  Lys  Thr  Cys  Phe  Arg  Cys
                      660                      665                      670

       Leu  Lys  Arg  Leu  Lys  Met  Ser  Trp  Phe  Leu  Pro  Thr  Val  Leu  Asp  Thr
                      675                      680                      685

       Gly  Gln  Gly  Phe  Lys  Leu  Val  Lys  Ser
            690                      695
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134

<210> 78
<211> 3008
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (372)..(2462)

<400> 78
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aaagtttacg ccgacactgg cctgtattag cgcgtatggc ctcgggccct cgttccccaa 120

ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcggtt aatttttgta acgtgaggga aaagcccaca 360

ttgctggtta c atg tgt aaa tca ctg cgt tat tgc ttt agt cat tgt ctc   410
              Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu
               1   5   10

tat tta gca atg aca aga ctg gaa gaa gta aat aga gaa gtg aac atg   458
Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met
     15   20   25

cat tct tca gtg cgg tat ctt ggc tat tta gcc aga atc aat tta ttg   506
His Ser Ser Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu
 30   35   40   45

gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat   554
Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn
             50   55   60

tcc tta att ttg gta att ttt att ctt ggt ctt ttt gtt ctt gga atc   602
Ser Leu Ile Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile
             65   70   75

gcc agc ata ctc tat tac tat ttt tca atg gaa gca gca agt tta agt   650
Ala Ser Ile Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser
         80   85   90

ctc tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt   698
Leu Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu
     95   100   105

gat aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat   746
Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr
110   115   120   125

ttg ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag   794
Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu

135

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aga att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt    842
Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val
            145               150               155

gaa ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg    890
Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu
        160               165               170

gtg gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg    938
Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met
        175               180               185

ctg att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta    986
Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu
190               195               200               205

gtt att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa   1034
Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys
                210               215               220

aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct   1082
Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro
            225               230               235

ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa   1130
Phe Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys
            240               245               250

ccc ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt   1178
Pro Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe
        255               260               265

gct gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt   1226
Ala Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu
270               275               280               285

aga gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt   1274
Arg Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe
            290               295               300

gga att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg   1322
Gly Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp
            305               310               315

gga ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac   1370
Gly Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His
            320               325               330

agg aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg   1418
Arg Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met
            335               340               345

cgc cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt   1466
Arg His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu
350               355               360               365
```

136

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gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att    1514
Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile
                370                 375                 380

ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat    1562
Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His
                385                 390                 395

ggg ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga    1610
Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly
            400                 405                 410

tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca    1658
Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro
        415                 420                 425

aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act    1706
Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr
430                 435                 440                 445

ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag    1754
Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu
                450                 455                 460

acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg    1802
Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu
            465                 470                 475

cat tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc    1850
His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro
        480                 485                 490

aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca    1898
Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr
        495                 500                 505

gga gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt    1946
Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu
510                 515                 520                 525

ata gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att    1994
Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile
                530                 535                 540

atc gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg    2042
Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg
                545                 550                 555

aaa att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa    2090
Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys
                560                 565                 570

aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca    2138
Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr
        575                 580                 585
```

137

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aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg   2186
Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp
590                 595                 600                 605

act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg   2234
Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg
                610                 615                 620

tgg agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag   2282
Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys
                625                 630                 635

cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg   2330
His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu
            640                 645                 650

gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt   2378
Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys
        655                 660                 665

ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg   2426
Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val
670                 675                 680                 685

ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac   2472
Leu Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
                690                 695

cccaaagcgg gatattaata agcactcata ctaccaatta tcactaactt gccatttttt 2532

gtatgctgta tttttatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg 2592

tcttttctta agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa 2652

gtatgtaggg agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca 2712

ctttcaggaa tgtttgctta tggtcctgat tagaaagaaa cagttgtcta tgctctgcaa 2772

tggtcaatga tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat 2832

gtagaccaga taaatttgtt tactgtttta agaaaactac cagtttactt acagaagatt 2892

cttttttcca aacagtaggt ttcatccaag accatttgaa gaactgcaaa ctctttctct 2952

tagaaaagaa agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac     3008


<210> 79
<211> 611
<212> PRT
<213> Homo sapiens

<400> 79
Met Glu Ala Ala Ser Leu Ser Leu Ser Asn Leu Trp Phe Gly Phe Leu
 1               5                   10                  15

Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser Ser Phe Lys Asn Asp Val
```

138

Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu Thr Ser Ile Val Leu Arg
    35   40   45

Ile Leu Cys Ser Leu Val Glu Arg Ile Ser Gly Tyr Val Arg His Arg
    50   55   60

Pro Thr Leu Leu Thr Thr Val Glu Phe Leu Glu Leu Val Gly Phe Ala
65   70   75   80

Ile Ala Ser Thr Thr Met Leu Val Glu Lys Ser Leu Ser Val Ile Leu
        85   90   95

Leu Val Val Ala Leu Ala Met Leu Ile Ile Asp Leu Arg Met Lys Ser
        100   105   110

Phe Leu Ala Ile Pro Asn Leu Val Ile Phe Ala Val Leu Leu Phe Phe
        115   120   125

Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile Ala Phe Ala Cys Phe Phe
        130   135   140

Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp Ile Tyr Phe Ser Gly Leu
145   150   155   160

Ser Val Thr Glu Arg Trp Lys Pro Phe Leu Tyr Arg Gly Arg Ile Cys
        165   170   175

Arg Arg Leu Ser Val Val Phe Ala Gly Met Ile Glu Leu Thr Phe Phe
        180   185   190

Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr His Leu Trp Tyr Phe Val
        195   200   205

Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe Trp Met Ile Cys His Ile
        210   215   220

Ile Phe Leu Leu Thr Leu Trp Gly Phe His Thr Lys Leu Asn Asp Cys
225   230   235   240

His Lys Val Tyr Phe Thr His Arg Thr Asp Tyr Asn Ser Leu Asp Arg
        245   250   255

Ile Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln
        260   265   270

Leu Val Phe Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser
        275   280   285

Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu
        290   295   300

Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys
305   310   315   320

Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe

139

Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln
            340   345   350

Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe
            355   360   365

Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser
    370   375   380

Gly Leu Ser Phe Asp Thr Leu His Ser Lys Leu Lys Ala Phe Leu Glu
385   390   395   400

Leu Arg Thr Val Asp Gly Pro Arg His Asp Thr Tyr Ile Leu Tyr Tyr
            405   410   415

Ser Gly His Thr His Gly Thr Gly Glu Trp Ala Leu Ala Gly Gly Asp
            420   425   430

Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp Trp Arg Glu Lys Asn Gly
            435   440   445

Ser Phe Cys Ser Arg Leu Ile Ile Val Leu Asp Ser Glu Asn Ser Thr
    450   455   460

Pro Trp Val Lys Glu Val Arg Lys Ile Asn Asp Gln Tyr Ile Ala Val
465   470   475   480

Gln Gly Ala Glu Leu Ile Lys Thr Val Asp Ile Glu Glu Ala Asp Pro
            485   490   495

Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp Val Glu Tyr Asn Cys Asn
            500   505   510

Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys Gly Arg Thr Val Lys Ala
            515   520   525

Val Tyr Gly Val Ser Lys Arg Trp Ser Asp Tyr Thr Leu His Leu Pro
    530   535   540

Thr Gly Ser Asp Val Ala Lys His Trp Met Leu His Phe Pro Arg Ile
545   550   555   560

Thr Tyr Pro Leu Val His Leu Ala Asn Trp Leu Cys Gly Leu Asn Leu
            565   570   575

Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys Leu Lys Arg Leu Lys Met
            580   585   590

Ser Trp Phe Leu Pro Thr Val Leu Asp Thr Gly Gln Gly Phe Lys Leu
            595   600   605

Val Lys Ser
610

<210> 80
<211> 3007
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (629)..(2461)

<400> 80
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aaagtttacg ccgacactgg cctgtattag cgcgtatggc ctcgggccct cgttccccaa 120

ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcggtt aatttttgta cgtgaggga aaagcccaca 360

ttgctggtta catgtgtaaa tcactgcgtt attgctttag tcattgtctc tatttagcaa 420

tgacaagact ggaagaagta aatagagaag tgaacatgca ttcttcagtg cggtatcttg 480

ctatttagcc agaatcaatt tattggttgc tatatgctta ggtctatacg taagatggga 540

aaaaacagca aattccttaa ttttggtaat ttttattctt ggtctttttg ttcttggaat 600

cgccagcata ctctattact attttttca atg gaa gca gca agt tta agt ctc   652
                                    Met Glu Ala Ala Ser Leu Ser Leu
                                     1   5

tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt gat   700
Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp
    10   15   20

aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg   748
Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu
 25   30   35   40

ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga   796
Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg
                45   50   55

att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa   844
Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu
            60   65   70

ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg   892
Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val
        75   80   85

gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg   940
Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu
    90   95   100

141

```
att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta gtt    988
Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val
105                     110                 115                 120

att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa aat   1036
Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn
                125                 130                 135

ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc   1084
Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe
                140                 145                 150

ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa ccc   1132
Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro
                155                 160                 165

ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt gct   1180
Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala
                170                 175                 180

gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt aga   1228
Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg
185                     190                 195                 200

gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt gga   1276
Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly
                205                 210                 \   215

att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg gga   1324
Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly
                220                 225                 230

ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac agg   1372
Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg
                235                 240                 245

aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg cgc   1420
Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg
                250                 255                 260

cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt gca   1468
His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala
265                     270                 275                 280

aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att ttc   1516
Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe
                285                 290                 295

ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat ggg   1564
Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly
                300                 305                 310

ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga tat   1612
Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr
                315                 320                 325
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142

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gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca aca    1660
Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr
    330             335             340

ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act ggc    1708
Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly
345             350             355             360

atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag acc    1756
Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr
                365             370             375

tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg cat    1804
Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His
            380             385             390

tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc aga    1852
Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg
        395             400             405

cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga    1900
His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly
    410             415             420

gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt ata    1948
Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile
425             430             435             440

gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att atc    1996
Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile
            445             450             455

gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa    2044
Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys
            460             465             470

att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa aca    2092
Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr
            475             480             485

gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca aaa    2140
Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys
    490             495             500

gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg act    2188
Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr
505             510             515             520

gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg tgg    2236
Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp
            525             530             535

agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag cac    2284
Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His
            540             545             550

tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg gca    2332
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    Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala
        555                 560                 565

aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt ttt   2380
Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe
    570                 575                 580

agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg ctg   2428
Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu
585                 590                 595                 600

gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac cccaaagcgg 2481
Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
                605                 610

gatattaata agcactcata ctaccaatta tcactaactt gccatttttt gtatgctgta 2541

tttttatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg tcttttctta 2601

agtaattatg gtatatataa ggcgttggga aaaacattt tataatgaaa gtatgtaggg  2661

agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca ctttcaggaa 2721

tgtttgctta tggtcctgat tagaaagaaa cagttgtcta tgctctgcaa tggtcaatga 2781

tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat gtagaccaga 2841

taaatttgtt tactgtttta agaaaactac cagtttactt acagaagatt ctttttcca  2901

aacagtaggt ttcatccaag accatttgaa gaactgcaaa ctctttctct tagaaaagaa 2961

agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac               3007


<210> 81
<211> 184
<212> PRT
<213> Homo sapiens

<400> 81
Met Thr Ser Phe Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu
 1               5                  10                  15

Gln Met Thr Val Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln
                20                  25                  30

Ser Ile Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys
            35                  40                  45

Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln
    50                  55                  60

Val Ser Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser
65                  70                  75                  80

Ser Val Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu
                85                  90                  95
```

```
Ile Val Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro
                100                 105                 110

Tyr Arg Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys
            115                 120                 125

Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser
    130                 135                 140

Pro Arg Ser Leu Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile
145                 150                 155                 160

Pro Glu Tyr Gly Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro
                165                 170                 175

Thr Glu Met Asp Glu Asn Glu Ser
            180
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<210> 82
<211> 1617
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (285)..(836)

<400> 82

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gcgcgcgcgg gagcgcggga ggatcggcgg ctcgcggtca ctggtccctg gctcggttcc 120

ccgcaccccg gggctcacac ttacccgcgc ggaggagcag cggccgggtg tccaccccca 180

tcctgcgccc agtctcctcg attcccctcg ctctgagccg ggagagccga acagctgaag 240

agagttcact gactccccag ccccaggtgg gccttgtgca catc atg acc agt ttt 296
                                              Met Thr Ser Phe
                                               1

gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt 344
Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val
  5                  10                  15                  20

tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt 392
Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe
                25                  30                  35

aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat 440
Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn
            40                  45                  50

tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt 488
Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val
        55                  60                  65
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145

```
cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc    536
Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser
     70               75              80

ttt gaa ata aaa aat atg agt aaa aag acc aat ctg atc gtg gac agc    584
Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser
 85               90              95              100

aga gag ctg ggc tac cta aat aaa atg gac ctg cca tac agg tgc atg    632
Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met
             105              110              115

gtc aga ttc gga gag tat cag ttt ctg atg gag aag gaa gat ggc gag    680
Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu
             120              125              130

tca ttg gaa ttt ttt gag act caa ttt att tta tct cca aga tca ctc    728
Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu
         135              140              145

ttg caa gaa aac aac tgg cca cca cac agg ccc ata ccg gag tat ggc    776
Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly
     150              155              160

act tat tcg ctc tgc tcc tcc caa agc agt tct ccg aca gaa atg gat    824
Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro Thr Glu Met Asp
165              170              175              180

gaa aat gag tca tgaacacaga aagtctaaga ggagaaatat gatggatgaa       876
Glu Asn Glu Ser

gagctctgta gatgctgtat agacactaaa taagagttga ttagggtagt atattatagt 936

catctgttat gctgtgaaat ttggaattca gtattatcat tttgaagtct gtaaattgtg 996

ttagtcatta acttagtcac ctgttgtatt ctggatctac acaaaattat tttaactgct 1056

cttattaatc tgtgaggatt aatatacaaa aagtatcctt tgagatgaag tcgtgttctc 1116

aaaataaggt tatattattt tcttttctg cttgattttc atcttgtgtt ttgctttgtt 1176

tttgtaagga accatctctt ggtttggtca catcagttca caacagccat ttgttttcaa 1236

ggtcaaggct ccaggcaggt tgttactggt gtttgcagcc tgtcagtact tgcagtactg 1296

gaataggttc taggctagtg tctgcgcgtc actgtggttt tagcatggga ggacttattt 1356

gagaaatact accttacttt tctatgattt cttttacag agttatagtg tgtttactcc 1416

taagatgaca gttctctttg tctatattca gcatctaaga caaatattta aacattttaa 1476

agaaccactg tgttaagttt aggattattt acttaccaaa ttagaagttt gacttttatg 1536

tgttatacac aatcttaaaa tttcacgaat tcacctttt aatagtatcc atgtacataa 1596

taaaatcaaa gtttaattag c                                          1617
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146

<210> 83
<211> 392
<212> PRT
<213> Homo sapiens

<400> 83
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1   5   10   15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
            20   25   30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
        35   40   45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
    50   55   60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65   70   75   80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
                85   90   95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
            100   105   110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
        115   120   125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
    130   135   140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145   150   155   160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
            165   170   175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
            180   185   190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
        195   200   205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
    210   215   220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225   230   235   240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
            245   250   255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

147

Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr
        275   280   285

Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu
    290   295   300

Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
305   310   315   320

Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
                325   330   335

Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
                340   345   350

Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg
                355   360   365

Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
    370   375   380

Val Glu Ser Pro Val Gln Lys Val
385   390

<210> 84
<211> 1898
<212> DNA
<213> Homo sapiens

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<222> (119)..(1294)

<400> 84
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cgcgcggccc ggggactcgc attccccggt tcccccctcca ccccacgcgg cctggacc   118

atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc   166
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1   5   10   15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc   214
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
                20   25   30

cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc   262
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
            35   40   45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac   310
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
        50   55   60

148

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-tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt    358
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65                  70                  75                  80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc    406
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
                85                  90                  95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg    454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
            100                 105                 110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg    502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
        115                 120                 125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca    550
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
    130                 135                 140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga    598
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145                 150                 155                 160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag    646
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
                165                 170                 175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc    694
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
            180                 185                 190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc    742
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
        195                 200                 205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg    790
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
    210                 215                 220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac    838
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225                 230                 235                 240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc    886
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
                245                 250                 255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc    934
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
            260                 265                 270

ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc    982
Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr
        275                 280                 285

cgc ttc atg ggg cga cac agt gag ttt gct gcc cat gcc ctg cta ctc   1030
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149

Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu
    290   295   300

tcc atc tgc tcc gca tgt ggc cag ctc ttc atc ttt tac acc att ggg   1078
Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
305   310   315   320

cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc   1126
Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
                325   330   335

ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg   1174
Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
            340   345   350

gtg gga ggg ctg ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga   1222
Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg
        355   360   365

gtc tac gcg cgg ggc cgt cta aag caa cgg gga aag aag gct gtg cct   1270
Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
    370   375   380

gtt gag tct cct gtg cag aag gtt tgagggtgga aagggcctga ggggtgaagt   1324
Val Glu Ser Pro Val Gln Lys Val
385   390

gaaataggac cctcccacca tccccttctg ctgtaacctc tgagggagct ggctgaaagg   1384

gcaaaatgca ggtgttttct cagtatcaca gaccagctct gcagcagggg attggggagc   1444

ccaggaggca gccttccctt ttgccttaag tcacccatct tccagtaagc agtttattct   1504

gagccccggg ggtagacagt cctcagtgag gggttttggg gagtttgggg tcaagagagc   1564

ataggtaggt tccacagtta ctcttcccac aagttccctt aagtcttgcc ctagctgtgc   1624

tctgccacct tccagactca ctcccctctg caaatacctg catttcttac cctggtgaga   1684

aaagcacaag cggtgtaggc tccaatgctg ctttcccagg agggtgaaga tggtgctgtg   1744

ctgaggaaag gggatgcaga gccctgccca gcaccaccac tcctatgct cctggatccc   1804

taggctctgt tccatgagcc tgttgcaggt tttggtactt tagaaatgta acttttttgct   1864

cttataattt tattttatta aattaaatta ctgc   1898

<210> 85
<211> 432
<212> PRT
<213> Homo sapiens

<400> 85
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
  1   5   10   15

150

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
                 20   25   30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
             35   40   45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
         50   55   60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65   70   75   80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
                 85   90   95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
             100   105   110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
         115   120   125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
    130   135   140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145   150   155   160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
                 165   170   175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
             180   185   190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
    195   200   205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
    210   215   220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225   230   235   240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
             245   250   255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
             260   265   270

Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
    275   280   285

Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
    290   295   300

Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
305   310   315   320

151

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Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
            325               330              335

Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
            340               345              350

Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
            355               360              365

Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
    370               375              380

Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
385               390               395              400

Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
            405               410              415

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
            420               425              430
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<210> 86
<211> 2018
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (119)..(1414)

<400> 86
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cgcgcggccc ggggactcgc attccccggt tccccctcca ccccacgcgg cctggacc    118

atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc   166
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1               5                  10                  15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc   214
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
            20                  25                  30

cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc   262
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
        35                  40                  45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac   310
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
    50                  55                  60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt   358
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65                  70                  75                  80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc   406
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    Val  Phe  Gly  Asn  Glu  Pro  Lys  Ala  Ser  Asp  Glu  Val  Pro  Leu  Ala  Pro
                            85                        90                   95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg        454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
            100                 105                 110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg        502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
            115                 120                 125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca        550
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
            130                 135                 140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga        598
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145                 150                 155                 160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag        646
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
                165                 170                 175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc        694
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
                180                 185                 190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc        742
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
                195                 200                 205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg        790
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
            210                 215                 220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac        838
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225                 230                 235                 240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc        886
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
                245                 250                 255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc        934
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
                260                 265                 270

atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg        982
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
                275                 280                 285

cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg cag atg atg ttt       1030
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
            290                 295                 300

ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa       1078
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
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153

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cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag   1126
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
            325                 330                 335

ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag   1174
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
            340                 345                 350

ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc   1222
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
            355                 360                 365

atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt   1270
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
        370                 375                 380

ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg   1318
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
385                 390                 395                 400

gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag   1366
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
            405                 410                 415

caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt   1414
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
            420                 425                 430

tgagggtgga aagggcctga ggggtgaagt gaaataggac cctcccacca tccccttctg   1474

ctgtaacctc tgagggagct ggctgaaagg gcaaaatgca ggtgttttct cagtatcaca   1534

gaccagctct gcagcagggg attggggagc ccaggaggca gccttccctt ttgccttaag   1594

tcacccatct tccagtaagc agtttattct gagccccggg ggtagacagt cctcagtgag   1654

gggttttggg gagtttgggg tcaagagagc ataggtaggt tccacagtta ctcttcccac   1714

aagttccctt aagtcttgcc ctagctgtgc tctgccacct tccagactca ctcccctctg   1774

caaatacctg catttcttac cctggtgaga aaagcacaag cggtgtaggc tccaatgctg   1834

ctttcccagg agggtgaaga tggtgctgtg ctgaggaaag gggatgcaga gccctgccca   1894

gcaccaccac tcctatgct cctggatccc taggctctgt tccatgagcc tgttgcaggt   1954

tttggtactt tagaaatgta acttttgct cttataattt tattttatta aattaaatta   2014

ctgc                                                              2018
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<210> 87
<211> 235
<212> PRT
<213> Homo sapiens

154

<400> 87
Met Gly Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser
 1   5   10   15

Trp Gly Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser
            20   25   30

Asp Ser Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His
            35   40   45

Ser Asn Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser
        50   55   60

Val Glu Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys
 65   70   75   80

Phe Val Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val
                85   90   95

Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe
            100   105   110

Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala
            115   120   125

Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu
            130   135   140

Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser
145   150   155   160

Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu
                165   170   175

Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile
            180   185   190

Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg
            195   200   205

Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu
            210   215   220

Thr Arg Asn Met Val Gln Arg Gln Phe Ile Ala
225   230   235

<210> 88
<211> 2717
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (111)..(815)

155

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aaaaggaaga cagaaaagcc gcgggctgac tgtggtggcg ctcgcctgca gattgaaaag 60

aaatgctgag aaatacataa agttttcctc ttctgccttg gatatttata atg ggt      116
                                                        Met Gly
                                                         1

atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt     164
Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly
         5               10                  15

aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc     212
Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser
     20                  25                  30

aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat     260
Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn
 35                  40                  45                  50

aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa     308
Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu
                 55                  60                  65

gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg     356
Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys Phe Val
                 70                  75                  80

ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat     404
Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn
             85                  90                  95

ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag     452
Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu
     100                 105                 110

atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat     500
Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn
115                 120                 125                 130

ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat     548
Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp
                 135                 140                 145

act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac     596
Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn
             150                 155                 160

agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat     644
Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn
         165                 170                 175

ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc     692
Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala
     180                 185                 190

tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt     740
Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe
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156

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cag gag tct gtg tat aag aca caa caa act ata tgg aaa gag aca aga  788
Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg
            215                 220                 225

aat atg gta caa aga caa ttt att gcc tgagatgaaa catataacat        835
Asn Met Val Gln Arg Gln Phe Ile Ala
            230                 235

gtggctggct cttgttttgt aaaccaaatg attaatcttc acttgagaaa gcagtttcta 895

ggaaatgttt aaataaaaga gagtcttcac cttaaagaaa cctatggagc acaagaaaga 955

taaatttctg caggacagcc tataaaattg tggtactttt tgatgtttca gtaaacttga 1015

cattgtcaga gtttcaagga cttttctttc acaattttcc tagttcatgg atatgaaaaa 1075

ggaattctca atccatattc cttgtattga accttgaaca aaaacttgta tgacagacat 1135

ttttaaaaat gtgacaacac ttttattctc tgaattttga tctcaaagga cacagaaaaa 1195

aaatggcccc aggagatctg atcacacttc ctcctgaggc acctctcatg gatgttgcaa 1255

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cttctaaaag gcgtataact gtgtgagtgg ccagatattc actttttaga tcaaaaacct 1615

ctcttatgga agctttaaaa gtttccgtca cacacaattc tcttctcagg aagtatttct 1675

catttaggtc ttcaaagtag cctgactgtg tgcatgtgtg tgtgtgatag gttatttata 1735

aagactttgg atagaaggag atgtatttta ttacctccta ttctagagcc ccatgctcct 1795

aacaagccag agaggcccca aacaggattg tttctttcct ccacagccct tctgcccatc 1855

tgagattgag ggagcatcgt ccacttgaga tcagggatgg ggtggagaat gggtcatgtc 1915

atgtaatgag aaaagccctc ttcgggatca tgagacttgg ttctagtcca atttctgcca 1975

ctgaggatga atgtaactgt gggcaaacta tttaccctcc tttatctgtg aaatgaaagg 2035

gttgaattga tggatctcta aaggcttttg tcctctatga ggatgtgaaa aactagggac 2095

cacaaaaggg aacaagcaaa aaagtttgga ttcgataaag tgatatgtaa tagttgcaga 2155

aggctttata tatgcttata atgaaaagat attttttgta tattgacagc ataatttatt 2215

tttaatgctg tcattacact taaagtcaca ggaaaaaaat atacatgctt actcaggctt 2275
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157

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tcttaaaaat aaatttttat agagatcctt gagtaaagac attttgctta atttcttttt 2335

tcttattccc cacttgtata tcccctacca gtaccgggat ctgcacacat ctttttgcag 2395

ttacctcttc atagccatga accaaaacgt tctatgagga gcatgcaagt aagtcaagcc 2455

tcctattctg ttagtactta ttagaggagg agatggtttt cattgcatag tgacattttc 2515

ttagccttaa cgttctgata gtagcttact actcacttct cttttcagt tttcataata 2575

agtattcatt tttttgccat aatgcttcct gtaaagccaa ttttatatac taataaaaca 2635

tgaactgccc actcttcatg cctgccaaac ttggggcaat tgatgctaaa tggtattttt 2695

aaaataaatg tttttattct tt                                      2717
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<210> 89
<211> 245
<212> PRT
<213> Homo sapiens

<400> 89
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Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
  1               5                  10                  15

Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
                 20                  25                  30

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
             35                  40                  45

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
         50                  55                  60

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe
 65                  70                  75                  80

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe
                 85                  90                  95

Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
                100                 105                 110

Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
            115                 120                 125

Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
        130                 135                 140

Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
145                 150                 155                 160

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
                165                 170                 175
```

158

```
Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
            180               185               190

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
            195               200               205

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu
            210               215               220

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn
225               230               235               240

Gln Tyr Glu Ile Val
                245


<210> 90
<211> 1793
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (60)..(794)

<400> 90
gcgtctcgct ctctgtgttc caatcgcccg gtgcggtggt gcagggtctc gggctagtc    59

atg gcg tcc ccg tct cgg aga ctg cag act aaa cca gtc att act tgt   107
Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
 1               5               10              15

ttc aag agc gtt ctg cta atc tac act ttt att ttc tgg atc act ggc   155
Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
            20              25              30

gtt atc ctt ctt gca gtt ggc att tgg ggc aag gtg agc ctg gag aat   203
Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
            35              40              45

tac ttt tct ctt tta aat gag aag gcc acc aat gtc ccc ttc gtg ctc   251
Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
        50              55              60

att gct act ggt acc gtc att att ctt ttg ggc acc ttt ggt tgt ttt   299
Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe
 65              70              75              80

gct acc tgc cga gct tct gca tgg atg cta aaa ctg tat gca atg ttt   347
Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe
            85              90              95

ctg act ctc gtt ttt ttg gtc gaa ctg gtc gct gcc atc gta gga ttt   395
Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
            100             105             110

gtt ttc aga cat gag att aag aac agc ttt aag aat aat tat gag aag   443
```

159

Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
        115   120   125

gct ttg aag cag tat aac tct aca gga gat tat aga agc cat gca gta   491
Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
    130   135   140

gac aag atc caa aat acg ttg cat tgt tgt ggt gtc acc gat tat aga   539
Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
145   150   155   160

gat tgg aca gat act aat tat tac tca gaa aaa gga ttt cct aag agt   587
Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
                165   170   175

tgc tgt aaa ctt gaa gat tgt act cca cag aga gat gca gac aaa gta   635
Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
            180   185   190

aac aat gaa ggt tgt ttt ata aag gtg atg acc att ata gag tca gaa   683
Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
            195   200   205

atg gga gtc gtt gca gga att tcc ttt gga gtt gct tgc ttc caa ctg   731
Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu
    210   215   220

att gga atc ttt ctc gcc tac tgc ctc tct cgt gcc ata aca aat aac   779
Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn
225   230   235   240

cag tat gag ata gtg taacccaatg tatctgtggg cctattcctc tctacctttg   834
Gln Tyr Glu Ile Val
                245

aggacattta gggtcccccc tgtgaattag aaagttgctt ggctggagaa ctgacaacac   894

tacttactga tagaccaaaa aactacacca gtaggttgat tcaatcaaga tgtatgtaga   954

cctaaaacta caccaatagg ctgattcaat caagatccgt gctcgcagtg ggctgattca   1014

atcaagatgt atgtttgcta tgttctaagt ccaccttcta tcccattcat gttagatcgt   1074

tgaaaccctg tatccctctg aaacactgga agagctagta aattgtaaat gaagtaatac   1134

tgtgttcctc ttgactgtta tttttcttag tagggggcct ttggaaggca ctgtgaattt   1194

gctattttga tgtagtgtta caagatggaa aattgattcc tctgactttg ctattgatgt   1254

agtgtgatag aaaattcacc cctctgaact ggctccttcc cagtcaaggt tatctggttt   1314

gattgtataa tttgcaccaa gaagttaaaa tgttttatga ctctctgttc tgctgacagg   1374

cagagagtca cattgtgtaa tttaatttca gtcagtcaat agatggcatc cctcatcagg   1434

gttgccagat ggtgataaca gtgtaaggcc ttgggtctaa ggcatccacg actggaaggg   1494

160

actactgatg ttctgtgata catcaggttt cagcacacaa cttacatttc tttgcctcca 1554

aattgaggca tttattatga tgttcatact ttccctcttg tttgaaagtt tctaattatt 1614

aaatggtgtc ggaattgttg tattttcctt aggaattcag tggaacttat cttcattaaa 1674

tttagctggt accaggttga tatgacttgt caatattatg gtcaacttta agtcttagtt 1734

ttcgtttgtg cctttgatta ataagtataa ctcttataca ataaatactg ctttcctct 1793

<210> 91
<211> 180
<212> PRT
<213> Homo sapiens

<400> 91
Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly
1   5   10   15

Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
            20   25   30

Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
        35   40   45

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
    50   55   60

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
65   70   75   80

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
                85   90   95

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
            100   105   110

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
            115   120   125

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
    130   135   140

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
145   150   155   160

Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
                165   170   175

Ala Leu Leu Gln
            180

<210> 92
<211> 970
<212> DNA

161

<213> Homo sapiens

<220>
<221> CDS
<222> (26)..(565)

<400> 92
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tttttcagct aaaggggaga tctgg atg gca tct act tcg tat gac tat tgc    52
                              Met Ala Ser Thr Ser Tyr Asp Tyr Cys
                               1               5

aga gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg   100
Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly
 10              15                  20                  25

ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg   148
Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu
                30                  35                  40

att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt   196
Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu
                45                  50                  55

cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag   244
Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu
        60                  65                  70

ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gct gcc   292
Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala
     75                  80                  85

acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag   340
Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu
 90                  95                 100                 105

aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act   388
Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr
                110                 115                 120

aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg   436
Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu
                125                 130                 135

aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac   484
Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr
        140                 145                 150

tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg   532
Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu
     155                 160                 165

att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 585
Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
170                 175                 180

acatcttgga aggtccgtcc tgctcggctt ttcgcttgaa cattcccttg atctcatcag 645
```

```
ttctgagcgg gtcatggggc aacacggtta gcggggagag cacggggtag ccggagaagg 705

gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 765

ttgacccagg gctgtctccc tccagagcct ccctccggac aatgagtccc ccctcttgtc 825

tcccaccctg agattgggca tggggtgcgg tgtggggggc atgtgctgcc tgttgttatg 885

ggtttttttt gcggggggg ttgctttttt ctggggtctt tgagctccaa aaaataaaca 945

cttcctttga gggagagcac acctt                                       970
```

<210> 93
<211> 331
<212> PRT
<213> Homo sapiens

<400> 93

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Met Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe
 1               5                  10                  15

Arg Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn
            20                  25                  30

Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu
        35                  40                  45

Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala
    50                  55                  60

Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp
 65                  70                  75                  80

Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile
                85                  90                  95

Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly
            100                 105                 110

Cys Thr Ile Ser Asn Val Val Ser Ser Thr Gly Ala Ala Ser Gly
            115                 120                 125

Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr
    130                 135                 140

Ser Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala
145                 150                 155                 160

Val Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser
                165                 170                 175

Ala Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu
            180                 185                 190

Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser
        195                 200                 205
```

163

```
Leu Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile
    210             215                 220

Arg Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr
225             230                 235                 240

Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala
                245                 250                 255

Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr
                260                 265                 270

Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu
            275                 280                 285

Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu
    290                 295                 300

Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln
305             310                 315                 320

Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His
                325                 330
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<210> 94
<211> 2039
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (175)..(1167)

<400> 94
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attatgcaga tgcacggctg gaggtgggat ccacacagct cagaacagct ggatcttgct 60

cacactcttt caagagaagc ttccttgggt taagaaaaaa aacgaaccct tccagtcagg 120

tcagtgactg gagagctcca aggaaagtct ctcagtgacc tggctgctgg cacc atg   177
                                                              Met
                                                              1

gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg   225
Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg
              5                  10                  15

gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa   273
Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu
         20                  25                  30

gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca   321
Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala
     35                  40                  45

gat gct ctc tac gaa gct ctg aag aag ctt aga aca tat gca gct att   369
```

Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala Ile
 50   55   60   65

gag gac gaa tat gtg cag cag aaa gat gag cag ttt agg gaa tgg ttt   417
Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp Phe
                      70   75   80

ttg aaa gag ttt ccc caa gtc aag agg aag atc cag gag tcc ata gaa   465
Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile Glu
                85   90   95

aag ctt cgt gcc ctt gca aat ggt att gaa gag gtc cac aga ggc tgc   513
Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly Cys
            100   105   110

acc atc tcc aac gtg gtg tcc agc tcc act ggc gct gcc tct ggc atc   561
Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly Ile
        115   120   125

atg tcc ctt gct ggt ctt gtt ttg gca cca ttt aca gca ggg acg agt   609
Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr Ser
130   135   140   145

ctg gcc ctt act gca gct ggg gta ggg ctg gga gca gcg tct gct gtg   657
Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala Val
                150   155   160

act ggg atc acc acc agc atc gtg gag cac tca tac aca tca tca gca   705
Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser Ala
                165   170   175

gaa gct gaa gcc agc agg ctg act gca acc agc att gac cga ttg aag   753
Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys
            180   185   190

gta ttt aag gaa gtt atg cgt gac atc aca ccc aac tta ctt tcc ctt   801
Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu
            195   200   205

ctt aat aat tat tac gaa gcc aca caa acc att ggg agt gaa atc cgt   849
Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile Arg
210   215   220   225

gcc atc agg caa gcc aga gcc agg gcc cga ctc cct gtg acc acc tgg   897
Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr Trp
                230   235   240

cga atc tca gct gga agt ggt ggt caa gca gag aga acg att gca ggc   945
Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala Gly
                245   250   255

acc acc cgg gca gtg agc aga gga gcc cgg atc ctg agt gcg acc act   993
Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr Thr
            260   265   270

tca ggc atc ttc ctt gca ctg gat gtg gtc aac ctt gta tac gag tca   1041
Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu Ser

165

```
aag cac ttg cat gag ggg gca aag tct gca tct gct gag gag ctg agg   1089
Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu Arg
290             295             300             305

cgg cag gct cag gag ctg gag gag aat cta atg gag ctc act cag atc   1137
Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln Ile
            310             315             320

tat cag cgt ctg aat cca tgc cat acc cac tgaccccaga ccagtgcagc    1187
Tyr Gln Arg Leu Asn Pro Cys His Thr His
            325             330

cagcagggga ggtgagccat acacaggcca cgacaaaatg caggcatttt attaggggga 1247

taaagagggc aaggtaaagt ttatggagct gagtgttagt gactttggca tttctgtagc 1307

tgagcacagc aggggagggg ttaatgcaga tggcaagtgc accaaggaga aggcaggaat 1367

gctggagcct ggaataaggg aggagagggg actggagagt gtggggaata ggaagaagaa 1427

atttccttta gactaacgaa tatattgggg ggaggaatag aggggaggtg tgcaggaacc 1487

agcaatgaga aggccaggaa agaaagagc tgaaaatgca gaaagccgaa gagttagaac 1547

ttttggatac agcagaagaa acagcggctc cactaccgac ctgcccccgg ttcgatgtcc 1607

ttccaagaat gaagtctttc cctggtgatg gtcccctgcc ctgtctttcc agcatccact 1667

ctgtcttgtc ctcctggaag tgtatctcag tcagccagtg gcttcttgat gatggcggtg 1727

gaggtggtgg ttgtagtgtg atggatcccc tttaggttat ttaggggtat atgtcccctg 1787

cttgaaccct gaaggccagg taatgagcca tggccattgt ccccagctga ggaccaggtg 1847

tctctaaaaa cccaaacatc ctggagagta tgcgagaacc taccagaaa aacagtctca 1907

ttactcatat acagcaggca aagagacaga aaattaactg aaaagcagtt tagagactgg 1967

gggaggccgg atctctagag ccatcctgct gagtgccctg tgtgtaagtc ctaataaact 2027

cacctactca cc                                                    2039
```

<210> 95
<211> 407
<212> PRT
<213> Homo sapiens

<400> 95

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Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu
  1               5                  10                  15

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys
                20                  25                  30
```

```
Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg
        35                    40                45

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
    50              55              60

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
65                  70              75                  80

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
                85              90              95

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
            100             105             110

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe
        115             120             125

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser
    130             135             140

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg
145             150             155             160

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
            165             170             175

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr
            180             185             190

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
    195             200             205

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
    210             215             220

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
225             230             235             240

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
            245             250             255

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
            260             265             270

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
    275             280             285

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
    290             295             300

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
305             310             315             320

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
            325             330             335


                                167
```

```
   Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
          340               345               350

Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
          355               360               365

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
    370               375               380

Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe
385               390               395               400

Val Cys Lys Tyr Lys Leu Leu
                405


<210> 96
<211> 1409
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (181)..(1401)

<400> 96
gctgtgcttg gcgcgtaccg tgcggtccct gtagttggag gacgggcggt cgcgcggcct 60

ttcccactag ccggagtagc ctctagttcg ttagtcaaaa cgtgaaaaaa aaagacctgc 120

tttgccctgg gaaatagtaa ccctgccaaa tacatcagct tgtaggagac agaggatgtg 180

atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgt agt ctg    228
Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu
  1               5                  10                  15

ttt gat gat cca cgg gtt ttg cct tgc tcc cac aac ttc tgc aaa aaa    276
Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys
                20                  25                  30

tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga    324
Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg
            35                  40                  45

cca gct cca ttc aag tgt cct aca tgc cgt aag gaa act tca gct act    372
Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
        50                  55                  60

gga att aat agc ctg cag gtt aat tac tcc ctg aag ggt att gtg gaa    420
Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
 65                  70                  75                  80

aag tat aac aag atc aag atc tct ccc aaa atg cca gta tgc aaa gga    468
Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
                85                  90                  95

cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg    516
```

168

```
        His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
                    100                 105                 110

att tgt ggg atc tgt gct act cgt ggg gag cac acc aaa cat gtc ttc    564
Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe
        115                 120                 125

tgt tct att gaa gat gcc tat gct cag gaa agg gat gcc ttt gag tcc    612
Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser
        130                 135                 140

ctc ttc cag agc ttt gag acc tgg cgt cgg gga gat gct ctt tct cgc    660
Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg
145                 150                 155                 160

ttg gat acc ttg gaa act agt aag agg aaa tcc cta cag tta ctg act    708
Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
                    165                 170                 175

aaa gat tca gat aaa gtg aag gaa ttt ttt gag aag tta caa cac aca    756
Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr
                    180                 185                 190

ctg gat caa aag aag aat gaa att ctg tct gac ttt gag acc atg aaa    804
Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
                195                 200                 205

ctt gct gtt atg caa gca tat gac cca gag atc aac aaa ctc aac acc    852
Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
        210                 215                 220

atc ttg cag gag caa cgg atg gcc ttt aac att gct gag gct ttc aaa    900
Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
225                 230                 235                 240

gat gtg tca gaa ccc att gta ttt ctg caa cag atg cag gag ttt aga    948
Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
                    245                 250                 255

gag aaa atc aaa gta atc aag gaa act cct tta cct ccc tct aat ttg    996
Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
                    260                 265                 270

cct gca agc cct tta atg aag aac ttt gat acc agt cag tgg gaa gac   1044
Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
                    275                 280                 285

ata aaa cta gtc gat gtg gat aaa ctt tct ttg cct caa gac act ggc   1092
Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
        290                 295                 300

aca ttc att agc aag att ccc tgg agc ttt tat aag tta ttt ttg cta   1140
Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
305                 310                 315                 320

atc ctt ctg ctt ggc ctt gtc att gtc ttt ggt cct acc atg ttc cta   1188
Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
```

169

```
gaa tgg tca tta ttt gat gac ctg gca act tgg aaa ggc tgt ctt tca    1236
Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
        340             345             350

aac ttc agt tcc tat ctg act aaa aca gcc gat ttc ata gaa caa tca    1284
Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
        355             360             365

gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa    1332
Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
        370             375             380

aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt    1380
Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe
385             390             395             400

gtg tgc aaa tat aaa cta tta taaaatcg                                1409
Val Cys Lys Tyr Lys Leu Leu
            405
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<210> 97
<211> 465
<212> PRT
<213> Homo sapiens

<400> 97
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Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys
 1               5                  10                  15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly
            20                  25                  30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser
            35                  40                  45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala
        50                  55                  60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu
65                  70                  75                  80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His
                85                  90                  95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys
            100                 105                 110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu
            115                 120                 125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val
        130                 135                 140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser
```

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg
            165   170   175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
            180   185   190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr
            195   200   205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn
    210   215   220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
225   230   235   240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
            245   250   255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
            260   265   270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
            275   280   285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
    290   295   300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
305   310   315   320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
            325   330   335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
            340   345   350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
            355   360   365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
            370   375   380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
385   390   395   400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
            405   410   415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
            420   425   430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
            435   440   445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly

171

Asp
465

<210> 98
<211> 1940
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (477)..(1871)

<400> 98
gttaacttcc tgacccagga agtggcagca acagagggga ctagcagcga atatacttta 60

caccaaatct cagaagattc agaacttaga tgagtggggc ccaggacagg aaccctggag 120

ccttggaagg aggggagccc catctcccca aagagcagt gaccccagca gagagggggcc 180

tggtgtatca ctggaggaaa tagcctgcca aggaatacac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgatc aaattgtgag aggaaaacag cctacccggt cctcttttct 300

tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420

tctggctgct tcatctccat ctctagagcc aatattggag cttttcaata aaagct atg 479
                                                                 Met
                                                                  1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc   527
Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser
              5   10   15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac   575
Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His
          20   25   30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa   623
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln
      35   40   45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca   671
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro
 50   55   60   65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att   719
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile
              70   75   80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga   767
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly
              85   90   95

172

```
gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg      815
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp
        100             105             110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt      863
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val
        115             120             125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag gaa gct gtg aca      911
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val Thr
130             135             140             145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca      959
Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr
            150             155             160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa     1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln
            165             170             175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa     1055
Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu
            180             185             190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg     1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu
        195             200             205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa     1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu
210             215             220             225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc     1199
Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala
            230             235             240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct     1247
Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala
            245             250             255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg     1295
Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met
        260             265             270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt     1343
Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser
        275             280             285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta     1391
His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu
290             295             300             305

att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag     1439
Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu
            310             315             320
```

173

```
aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg   1487-
Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu
            325             330             335

ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt   1535
Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val
            340             345             350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag   1583
Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln
            355             360             365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc   1631
Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu
370             375             380             385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act   1679
Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr
            390             395             400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac   1727
Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp
            405             410             415

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac   1775
Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His
            420             425             430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat   1823
Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr
435             440             445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac   1871
Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp
450             455             460             465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931

taagggcag                                                          1940


<210> 99
<211> 465
<212> PRT
<213> Homo sapiens

<400> 99
Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys
 1               5                   10                  15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly
            20                  25                  30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser
            35                  40                  45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala
```

174

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu
65   70   75   80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His
    85   90   95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys
   100   105   110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu
   115   120   125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val
   130   135   140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser
145   150   155   160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg
   165   170   175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
   180   185   190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr
   195   200   205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn
   210   215   220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
225   230   235   240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
   245   250   255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
   260   265   270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
   275   280   285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
   290   295   300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
305   310   315   320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
   325   330   335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
   340   345   350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val

175

```
Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
    370             375             380
```

```
Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
385             390             395             400
```

```
Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
            405             410             415
```

```
Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
            420             425             430
```

```
His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
            435             440             445
```

```
Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
    450             455             460
```

```
Asp
465
```

```
<210> 100
<211> 1940
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (477)..(1871)

<400> 100
gttaacttcc tgacccagga agtggcagca acagagggga ctagcagcga atatacttta   60

caccaaatct cagaagattc agaacttaga tgagtggggc ccaggacagg aaccctggag  120

ccttggaagg aggggagccc catctcccca gaagagcagt gaccccagca gagagggcc  180

tggtgtatca ctggaggaaa tagcctgcca aggaatacac gtcttcagaa gaagttctgt  240

gtggcttcaa gagactgatc aaattgtgag aggaaaacag cctacccggt cctctttct  300

tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag  360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat  420

tctggctgct tcatctccat ctctagagcc aatattggag cttttcaata aaagct atg  479
                                                              Met
                                                                1
```

```
gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc   527
Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser
              5                  10                  15
```

```
atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac   575
```

176

```
Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His
        20                  25                  30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa    623
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln
        35                  40                  45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca    671
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro
 50                  55                  60                      65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att    719
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile
                70                  75                  80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga    767
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly
                85                  90                  95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg    815
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp
            100                 105                 110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt    863
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val
        115                 120                 125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag aaa gct gtg aca    911
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val Thr
130                 135                 140                 145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca    959
Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr
                150                 155                 160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa   1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln
                165                 170                 175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa   1055
Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu
            180                 185                 190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg   1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu
        195                 200                 205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa   1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu
210                 215                 220                 225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc   1199
Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala
                230                 235                 240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct   1247
Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala
```

```
gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg    1295
Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met
        260             265             270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt    1343
Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser
        275             280             285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta    1391
His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu
290             295             300             305

att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag    1439
Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu
                310             315             320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg    1487
Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu
                325             330             335

ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt    1535
Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val
        340             345             350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag    1583
Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln
        355             360             365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc    1631
Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu
370             375             380             385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act    1679
Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr
                390             395             400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac    1727
Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp
            405             410             415

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac    1775
Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His
        420             425             430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat    1823
Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr
        435             440             445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac    1871
Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp
450             455             460             465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931

taagggcag                                                          1940
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178

<210> 101
<211> 685
<212> PRT
<213> Homo sapiens

<400> 101
Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys
 1   5   10   15

Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys
                20   25   30

Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln
            35   40   45

Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His
        50   55   60

Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys
 65   70   75   80

Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys
                85   90   95

Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile
            100   105   110

Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp
            115   120   125

Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln
        130   135   140

Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu
145   150   155   160

Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val
                165   170   175

Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly
            180   185   190

Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu
            195   200   205

Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe
    210   215   220

Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile
225   230   235   240

Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly
                245   250   255

His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr

179

Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr
  275   280   285

Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu
  290   295   300

Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu
305   310   315   320

Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln
    325   330   335

Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro
   340   345   350

Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala
   355   360   365

Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr
  370   375   380

His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His
385   390   395   400

Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr
    405   410   415

Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr
   420   425   430

Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile
  435   440   445

Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu
  450   455   460

Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg
465   470   475   480

Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln
   485   490   495

Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn
   500   505   510

Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu
   515   520   525

Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val
  530   535   540

His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp
545   550   555   560

Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser

180

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
        580   585   590

Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
      595   600   605

Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
      610   615   620

Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
625   630   635   640

Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
         645   650   655

Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg
        660   665   670

Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
      675   680   685

<210> 102
<211> 2783
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (128)..(2182)

<400> 102
gcacaagtgg accgggggtgt tgggtgctag tcggcaccag aggcaagggt gcgaggacca 60

cggccggctc ggacgtgtga ccgcgcctag ggggtggcag cgggcagtgc ggggcggcaa 120

ggcgacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc   169
       Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser
       1   5   10

acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg   217
Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser
15   20   25   30

aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct cag   265
Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln
          35   40   45

tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cac cat   313
Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His His
          50   55   60

tcg cac tcg ggg ccg gag atc tcg cgg att atc gtc gac ccc acg act   361
Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr
          65   70   75

181

```
ggg aag cgc tac tgc cgg ggc aaa gtg ctg gga aag ggt ggc ttt gca      409
Gly Lys Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala
     80                  85                  90

aaa tgt tac gag atg aca gat ttg aca aat aac aaa gtc tac gcc gca      457
Lys Cys Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala
 95                 100                 105                 110

aaa att att cct cac agc aga gta gct aaa cct cat caa agg gaa aag      505
Lys Ile Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys
                115                 120                 125

att gac aaa gaa ata gag ctt cac aga att ctt cat cat aag cat gta      553
Ile Asp Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val
            130                 135                 140

gtg cag ttt tac cac tac ttc gag gac aaa gaa aac att tac att ctc      601
Val Gln Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu
            145                 150                 155

ttg gaa tac tgc agt aga agg tca atg gct cat att ttg aaa gca aga      649
Leu Glu Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg
        160                 165                 170

aag gtg ttg aca gag cca gaa gtt cga tac tac ctc agg cag att gtg      697
Lys Val Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val
175                 180                 185                 190

tct gga ctg aaa tac ctt cat gaa caa gaa atc ttg cac aga gat ctc      745
Ser Gly Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu
                195                 200                 205

aaa cta ggg aac ttt ttt att aat gaa gcc atg gaa cta aaa gtt ggg      793
Lys Leu Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly
                210                 215                 220

gac ttc ggt ctg gca gcc agg cta gaa ccc ttg gaa cac aga agg aga      841
Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg
            225                 230                 235

acg ata tgt ggt acc cca aat tat ctc tct cct gaa gtc ctc aac aaa      889
Thr Ile Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys
        240                 245                 250

caa gga cat ggc tgt gaa tca gac att tgg gcc ctg ggc tgt gta atg      937
Gln Gly His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met
255                 260                 265                 270

tat aca atg tta cta ggg agg ccc cca ttt gaa act aca aat ctc aaa      985
Tyr Thr Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys
                275                 280                 285

gaa act tat agg tgc ata agg gaa gca agg tat aca atg ccg tcc tca     1033
Glu Thr Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser
                290                 295                 300
```

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ttg ctg gct cct gcc aag cac tta att gct agt atg ttg tcc aaa aac    1081
Leu Leu Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn
        305                 310                 315

cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac ttt ttt    1129
Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe
        320                 325                 330

ttg cag ggc ttc act ccg gac aga ctg tct tct agc tgt tgt cat aca    1177
Leu Gln Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr
335                 340                 345                 350

gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa    1225
Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys
                355                 360                 365

gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att    1273
Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile
                370                 375                 380

gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt    1321
Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu
                385                 390                 395

agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac    1369
Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His
        400                 405                 410

agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct    1417
Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser
415                 420                 425                 430

gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg    1465
Gly Thr Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg
                435                 440                 445

atg ata gtc aga ggg act ctt ggc agc tgt agc agc agc agt gaa tgc    1513
Met Ile Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys
                450                 455                 460

ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt    1561
Leu Glu Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val
        465                 470                 475

ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa    1609
Leu Arg Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys
        480                 485                 490

gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac    1657
Glu Gln Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr
495                 500                 505                 510

tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt    1705
Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly
                515                 520                 525

gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa    1753
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183

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  Val—Leu Phe Asn Asn Gly Ala—His Met Ser Leu Leu Pro Asp—Lys Lys
          530             535             540

aca gtt cac tat tac gca gag ctt ggc caa tgc tca gtt ttc cca gca  1801
Thr Val His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala
        545             550             555

aca gat gct cct gag caa ttt att agt caa gtg acg gtg ctg aaa tac  1849
Thr Asp Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr
    560             565             570

ttt tct cat tac atg gag gag aac ctc atg gat ggt gga gat ctg cct  1897
Phe Ser His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro
575             580             585             590

agt gtt act gat att cga aga cct cgg ctc tac ctc ctt cag tgg cta  1945
Ser Val Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu
            595             600             605

aaa tct gat aag gcc cta atg atg ctc ttt aat gat ggc acc ttt cag  1993
Lys Ser Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln
            610             615             620

gtg aat ttc tac cat gat cat aca aaa atc atc atc tgt agc caa aat  2041
Val Asn Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn
        625             630             635

gaa gaa tac ctt ctc acc tac atc aat gag gat agg ata tct aca act  2089
Glu Glu Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr
    640             645             650

ttc agg ctg aca act ctg ctg atg tct ggc tgt tca tca gaa tta aaa  2137
Phe Arg Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys
655             660             665             670

aat cga atg gaa tat gcc ctg aac atg ctc tta caa aga tgt aac  2182
Asn Arg Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
            675             680             685

tgaaagactt ttcgaatgga ccctatggga ctcctctttt ccactgtgag atctacaggg 2242

aacccaaaag aatgatctag agtatgttga agaagatgga catgtggtgg tacgaaaaca 2302

attcccctgt ggcctgctgg actgggtgga accagaacag gctaaggcat acagttcttg 2362

actttggaca atccaagagt gaaccagaat gcagttttcc ttgagatacc tgttttaaaa 2422

ggttttcag acaattttgc agaaaggtgc attgattctt aaattctctc tgttgagagc 2482

atttcagcca gaggactttg gaactgtgaa tatacttcct gaaggggagg gagaagggag 2542

gaagctccca tgttgtttaa aggctgtaat tggagcagct tttggctgcg taactgtgaa 2602

ctatggccat atataatttt ttttcattaa tttttgaaga tacttgtggc tggaaaagtg 2662

cattccttgt taataaactt tttatttatt acagcccaaa gagcagtatt tattatcaaa 2722
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184

<210> 103
<211> 161
<212> PRT
<213> Homo sapiens

<400> 103
Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala
 1   5   10   15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr
            20   25   30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val
            35   40   45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
    50   55   60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
 65   70   75   80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys
                85   90   95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
            100   105   110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
            115   120   125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
            130   135   140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
145   150   155   160

Leu

<210> 104
<211> 1589
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (70)..(552)

<400> 104
ccttttctcg gggcgcccga aggccagctc agacctcccg gctcgacagg cggcgcgggc 60

185

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       ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111
                 Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser
                  1           5                   10

       tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac   159
       Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
        15              20                  25                      30

       agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg   207
       Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
                        35                  40                  45

       ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat   255
       Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
                    50                  55                  60

       acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg   303
       Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
                65                  70                  75

       gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct atc caa atg   351
       Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met
            80                  85                  90

       tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac   399
       Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
        95              100                 105                 110

       gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg   447
       Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
                    115                 120                 125

       tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag   495
       Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
                    130                 135                 140

       gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac   543
       Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
                145                 150                 155

       aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg          592
       Lys Arg Leu
            160

       aagtcctttc cacctctcat ccagcttcac gcctggtgga ggttctgccc tggtggtctc 652

       acctctccag ggggcccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac 712

       aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

       cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtcc tgccatctaa 832

       ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctcttttttc 892

       ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952

       ttgaggctgt tctgcccaga gctcggctga accagccttt agtgcctacc attatcttat 1012
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186

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ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072

tgagattctg taactgcaga cttcattagc acacagattc actttaattt cttaattttt 1132

tttttaaata caaggagggg gctattaaca cccagtacag acatatccac aaggtcgtaa 1192

atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgtttctctg 1252

tgccagatct tcagtgcccc tttccataca gggatttttt tctcatagag taattatatg 1312

aacagttttt atgacctcct tttggtctga aatactttcg aacagaattt ctttttttta 1372

aaaaaaaaca gagatggggt cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432

aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492

tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552

tggtgtcatt ttcccatttg ccaatgtagt ctcactt                             1589


<210> 105
<211> 161
<212> PRT
<213> Homo sapiens

<400> 105
Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala
 1               5                  10                  15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr
            20                  25                  30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val
            35                  40                  45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
        50                  55                  60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
 65                  70                  75                  80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met Cys Cys
                85                  90                  95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
            100                 105                 110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
            115                 120                 125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
        130                 135                 140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
145                 150                 155                 160
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187

Leu

<210> 106
<211> 1589
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (70)..(552)

<400> 106
cctttctcg gggcgcccga aggccagctc agacctcccg gctcgacagg cggcgcgggc 60

ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111
           Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser
           1   5   10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159
Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
 15   20   25   30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207
Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
           35   40   45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255
Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
          50   55   60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303
Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
        65   70   75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct gtc caa atg 351
Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met
   80   85   90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399
Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
 95   100   105   110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447
Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
           115   120   125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495
Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
          130   135   140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543
Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
       145   150   155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592
Lys Arg Leu
    160

aagtcctttc cacctctcat ccagcttcac gcctggtgga ggttctgccc tggtggtctc 652

acctctccag ggggcccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac 712

aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtcc tgccatctaa 832

ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctctttttc 892

ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952

ttgaggctgt tctgcccaga gctcggctga accagccttt agtgcctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072

tgagattctg taactgcaga cttcattagc acacagattc actttaattt cttaattttt 1132

tttttaaata caaggagggg gctattaaca cccagtacag acatatccac aaggtcgtaa 1192

atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgtttctctg 1252

tgccagatct tcagtgcccc tttccataca gggatttttt tctcatagag taattatatg 1312

aacagttttt atgacctcct tttggtctga aatactttcg aacagaattt cttttttta 1372

aaaaaaaaca gagatggggt cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432

aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492

tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552

tggtgtcatt ttcccatttg ccaatgtagt ctcactt 1589

<210> 107
<211> 249
<212> PRT
<213> Homo sapiens

<400> 107
Met Ala Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val
 1   5   10   15

Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val
            20   25   30

Val Thr Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys
            35   40   45

Phe Lys Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn
    50   55   60

189

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Ser Gly Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu
 65                  70                  75                  80

Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met
                 85                  90                  95

Val Gln Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val
                100                 105                 110

Trp Lys Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys
            115                 120                 125

Val Phe Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro
130                 135                 140

Ser Lys Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro
145                 150                 155                 160

Lys Pro His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met
                165                 170                 175

Glu Glu Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu
            180                 185                 190

Asn Arg His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His
            195                 200                 205

Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val
210                 215                 220

Thr Ser Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile
225                 230                 235                 240

Gly Phe Phe Leu Gly Lys Phe Ile Leu
                245
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<210> 108
<211> 1595
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (232)..(978)

<400> 108
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agtgcgcgtg gccgtggcgg ctggtgtggg gttgagtcag ttgtgggacc cggagctgct 60

gacccagcgg gtggcccacc gaaccggtga cacagcggca ggcgttaggg ctcgggagcc 120

gcgagcctgg cctcgtccta gagctcggcc gagccgtcgc cgccgtcgtc ccccgccccc 180

agtcagcaaa ccgccgccgc gggcgcgccc ccgctctgcg ctgtctctcc g atg gcg 237
                                                          Met Ala
                                                           1
```

190

```
tcc gcc tca ggg gcc atg gcg aag cac gag cag atc ctg gtc ctc gat     285
Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp
          5               10                  15

ccg ccc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act     333
Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr
         20                  25                  30

aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa     381
Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys
     35                  40                  45                  50

gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga     429
Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly
                 55                  60                  65

att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc     477
Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro
             70                  75                  80

ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag     525
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln
             85                  90                  95

aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa     573
Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys
     100                 105                 110

gag gca aaa cct gat gaa tta atg gat tcc aaa ttg aga tgc gta ttt     621
Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe
115                 120                 125                 130

gaa atg ccc aat gaa aat gat aaa ttg aat gat atg gaa cct agc aaa     669
Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys
                 135                 140                 145

gct gtt cca ctg aat gca tct aag caa gat gga cct atg cca aaa cca     717
Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro
             150                 155                 160

cac agt gtt tca ctt aat gat acc gaa aca agg aaa cta atg gaa gag     765
His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu
         165                 170                 175

tgt aaa aga ctt cag gga gaa atg atg aag cta tca gaa gaa aat cgg     813
Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg
     180                 185                 190

cac ctg aga gat gaa ggt tta agg ctc aga aag gta gca cat tcg gat     861
His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp
195                 200                 205                 210

aaa cct gga tca acc tca act gca tcc ttc aga gat aat gtc acc agt     909
Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser
                 215                 220                 225

cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc     957
```

191

Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe
        230   235   240

ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttctt   1008
Phe Leu Gly Lys Phe Ile Leu
        245

tttttttttt tctcttgacc agaaaaagat ttgtttacct accatttcat tggtagtatg 1068

gcccacggtg accatttttt tgtgtgtaca gcgtcatata ggctttgcct ttaatgatct 1128

cttacggtta gaaaacacaa taaaaacaaa ctgttcggct actggacagg ttgtatatta 1188

ccagatcatc actagcagat gtcagttgca cattgagtcc tttatgaaat tcataaataa 1248

agaattgttc tttctttgtg gttttaataa gagttcaaga attgttcaga gtcttgtaaa 1308

tgttatttta ataatccctt taaattttat ctgttgctgt tacctcttga aatatgattt 1368

atttagattg ctaatcccac tcattcagga aatgccaaga ggtattcctt ggggaaatgg 1428

tgcctcttac agtgtaaatt tttcctcctt tacctttgct aatatcatgg cagaattttt 1488

cttatccctt gtgaggcagt tgttgactga gtttttcatc cttacaatcc tgtcccatgg 1548

tatttaacat aaaaaaaaat aaaactgtta acagattctt gctcgat   1595

<210> 109
<211> 540
<212> PRT
<213> Homo sapiens

<400> 109
Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
 1   5   10   15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
            20   25   30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
         35   40   45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
     50   55   60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
 65   70   75   80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
                85   90   95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
            100   105   110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
         115   120   125

192

```
Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
    130             135             140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
145             150             155             160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
            165             170             175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
            180             185             190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
            195             200             205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
    210             215             220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225             230             235             240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
            245             250             255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
            260             265             270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
            275             280             285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
    290             295             300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305             310             315             320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
            325             330             335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
            340             345             350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
            355             360             365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
    370             375             380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385             390             395             400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg
            405             410             415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
            420             425             430
```

193

```
Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
    435                 440                 445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
    450                 455                 460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
465                 470                 475                 480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
                485                 490                 495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
            500                 505                 510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
        515                 520                 525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu
    530                 535                 540


<210> 110
<211> 1810
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (102)..(1721)

<400> 110
aaccgtaaca gccaccagac aagcttcagt ggccggccct tcacatccag acttgcctga  60

gaggacccac ctctgagtgt ccagtggtca gttgccccag g atg ggg acc aca gcc  116
                                             Met Gly Thr Thr Ala
                                               1               5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct  164
Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser
            10                  15                  20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac  212
Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His
            25                  30                  35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga  260
Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg
        40                  45                  50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt  308
Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe
    55                  60                  65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct  356
Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro
```

194

```
ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa   404
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu
                90              95              100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg   452
Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu
            105             110             115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca   500
Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro
            120             125             130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag   548
Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln
    135             140             145

cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat   596
His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp
150             155             160             165

ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc   644
Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys
            170             175             180

ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag   692
Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln
            185             190             195

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg   740
Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu
            200             205             210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc   788
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg
    215             220             225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt   836
Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys
230             235             240             245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg   884
Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg
            250             255             260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca   932
Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro
            265             270             275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg   980
His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser
            280             285             290

ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc   1028
Gly Leu Glu Leu P
ro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile
```

195

```
aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg    1076
Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu
310             315             320             325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg    1124
Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu
            330             335             340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt    1172
Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys
            345             350             355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag    1220
Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu
            360             365             370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc    1268
Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser
    375             380             385

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat    1316
Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr
390             395             400             405

gac cgg gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc    1364
Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu
            410             415             420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat    1412
Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His
            425             430             435

att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca    1460
Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro
            440             445             450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc    1508
Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile
    455             460             465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc    1556
Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu
470             475             480             485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc    1604
Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile
            490             495             500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc    1652
Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala
            505             510             515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc    1700
Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser
    520             525             530
```

196

```
acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga        1751
Thr Ser Glu Pro Lys Glu Glu
    535                 540

tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg  1810
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<210> 111
<211> 540
<212> PRT
<213> Homo sapiens

<400> 111

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Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
 1               5                  10                  15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
            20                  25                  30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
        35                  40                  45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
    50                  55                  60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
 65                  70                  75                  80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
                85                  90                  95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
            100                 105                 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
        115                 120                 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
    130                 135                 140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
145                 150                 155                 160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
                165                 170                 175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
            180                 185                 190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
        195                 200                 205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
    210                 215                 220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
```

197

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
            245   250   255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
            260   265   270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
            275   280   285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
    290   295   300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305   310   315   320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
            325   330   335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
            340   345   350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
            355   360   365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
    370   375   380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385   390   395   400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg
            405   410   415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
            420   425   430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
    435   440   445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
    450   455   460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
465   470   475   480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
            485   490   495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
            500   505   510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
    515   520   525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu

198

<210> 112
<211> 1810
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (102)..(1721)

<400> 112
aaccgtaaca gccaccagac aagcttcagt ggccggccct tcacatccag acttgcctga 60

gaggacccac ctctgagtgt ccagtggtca gttgccccag g atg ggg acc aca gcc 116
                                             Met Gly Thr Thr Ala
                                             1   5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct   164
Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser
              10   15   20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac   212
Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His
          25   30   35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga   260
Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg
          40   45   50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt   308
Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe
      55   60   65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct   356
Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro
70   75   80   85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa   404
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu
              90   95   100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg   452
Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu
              105   110   115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca   500
Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro
              120   125   130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag   548
Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln
      135   140   145

cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat   596
His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp

199

```
ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc    644
Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys
            170             175             180

ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag    692
Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln
            185             190             195

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg    740
Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu
            200             205             210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc    788
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg
    215             220             225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt    836
Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys
230             235             240             245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg    884
Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg
            250             255             260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca    932
Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro
            265             270             275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg    980
His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser
            280             285             290

ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc    1028
Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile
    295             300             305

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg    1076
Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu
310             315             320             325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg    1124
Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu
            330             335             340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt    1172
Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys
            345             350             355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag    1220
Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu
            360             365             370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc    1268
Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser
    375             380             385
```

```
cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat    1316
Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr
390               395           400           405

gac cgg gac atc ttg acc att gac atc agt cga gtc acc ccc aac ctc    1364
Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg Val Thr Pro Asn Leu
              410           415           420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat    1412
Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His
              425           430           435

att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca    1460
Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro
          440           445           450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc    1508
Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile
      455           460           465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc    1556
Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu
470           475           480           485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc    1604
Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile
              490           495           500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc    1652
Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala
              505           510           515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc    1700
Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser
          520           525           530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga       1751
Thr Ser Glu Pro Lys Glu Glu
          535           540

tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg   1810


<210> 113
<211> 382
<212> PRT
<213> Homo sapiens

<400> 113
Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu Asp Lys Val Gln Ala
 1               5                   10                  15

Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe
            20                  25                  30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu
```

201

```
Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val
    50                  55              60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
65              70              75                          80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
                85              90              95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
            100             105             110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
        115             120             125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
    130             135             140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145             150             155             160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
            165             170             175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
            180             185             190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
    195             200             205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
    210             215             220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
225             230             235             240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
            245             250             255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
            260             265             270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
    275             280             285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
    290             295             300

Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
305             310             315             320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
            325             330             335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
```

202

```
        Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
                355                     360                 365

        Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
                370                     375                 380
```

<210> 114
<211> 3074
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (201)..(1346)

<400> 114
aactttacg aggtatcagc acttttcttt cattaggggg aaggcgtgag gaaagtacca 60

aacagcagcg gagtttttaaa ctttaaatag acaggtctga gtgcctgaac ttgccttttc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233
                        Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu
                         1   5   10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca   281
Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser
            15   20   25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca   329
Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser
        30   35   40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct   377
Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro
    45   50   55

ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg   425
Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val
60   65   70   75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg   473
Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu
            80   85   90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac   521
Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn
                95   100   105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg   569
Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val
            110   115   120

203

```
gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att   617
Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile
    125             130             135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac   665
Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr
140             145             150             155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg   713
Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu
            160             165             170

atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc   761
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys
            175             180             185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc   809
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro
            190             195             200

acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg   857
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val
    205             210             215

tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc   905
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly
220             225             230             235

gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt   953
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser
            240             245             250

ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat   1001
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr
            255             260             265

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct   1049
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro
            270             275             280

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc   1097
Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg
    285             290             295

aat tac aac aag caa gca agt gag caa acc tgg gct aat tac agt gca   1145
Asn Tyr Asn Lys Gln Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala
300             305             310             315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat   1193
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His
            320             325             330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta   1241
Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu
            335             340             345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct   1289
```

```
    Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro  —   —    —    —    —     --
           350                355                360

    tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac     1337
    Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp
       365                370            ·        375

    ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt            1386
    Leu Glu Ile
    380

    ggagaagaaa aaaggtgctg tagaaagtgc accaggtgtt aattttgatc cggtggaggt   1446

    ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt   1506

    tcactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg   1566

    gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata   1626

    catagataag ggcttttct ccccgcaaac accctaaga atggttctgt gtatgtgaat     1686

    gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg   1746

    ccaggaataa atacttcctg aacatcttag gtcttttcaa caagaaaaag acagaggatt   1806

    gtccttaagt ccctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt   1866

    ctaggcctga ccctccaggt gtcaatggac ttgtgctact atattttttt attcttggta   1926

    tcagtttaaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt   1986

    atattctttt tccatccact tgcacaatat cattaccatc acttttcat  cattcctcag    2046

    ctactactca cattcattta atggtttctg taaacatttt taagacagtt gggatgtcac   2106

    ttaacatttt ttttttgagc taaagtcagg gaatcaagcc atgcttaata tttaacaatc   2166

    acttatatgt gtgtcgaaga gtttgttttg tttgtcatgt attggtacaa gcagatacag   2226

    tataaactca caaacacaga tttgaaaata atgcacatat ggtgttcaaa tttgaacctt   2286

    tctcatggat ttttgtggtg tgggccaata tggtgtttac attatataat tcctgctgtg   2346

    gcaagtaaag cacacttttt ttttctccta aaatgttttt ccctgtgtat cctattatgg   2406

    atactggttt tgttaattat gattctttat tttctctcct tttttagga tatagcagta    2466

    atgctattac tgaaatgaat ttccttttc  tgaaatgtaa tcattgatgc ttgaatgata    2526

    gaattttagt actgtaaaca ggctttagtc attaatgtga gagacttaga aaaaaatgct   2586

    tagagtggac tattaaatgt gcctaaatga attttgcagt aactggtatt cttgggtttt   2646

    cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtcttttgg   2706

    agtgaccagc aactttgatg tttgcactaa gattttattt ggaatgcaag agaggttgaa   2766
```

205

```
__agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826

cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

tgacactttt cttcttgcat gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

ctaatttgtt tgacattcca tgttaaacta cggtcatgtt cagcttcatt gcatgtaatg 3006

tagacctagt ccatcagatc atgtgttctg gagagtgttc tttattcaat aaagttttaa 3066

tttagtat                                                             3074
```

<210> 115
<211> 382
<212> PRT
<213> Homo sapiens

<400> 115

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Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu Asp Lys Val Gln Ala
 1               5                  10                  15

Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe
            20                  25                  30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu
        35                  40                  45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val
    50                  55                  60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
65                  70                  75                  80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
                85                  90                  95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
               100                 105                 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
           115                 120                 125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
    130                 135                 140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145                 150                 155                 160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
                165                 170                 175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
            180                 185                 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
        195                 200                 205
```

206

```
Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
    210             215             220
Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
225             230             235             240
Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
            245             250             255
Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
            260             265             270
Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
            275             280             285
Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
    290             295             300
Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
305             310             315             320
Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
            325             330             335
Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
            340             345             350
Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
    355             360             365
Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
    370             375             380
```

<210> 116
<211> 3074
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (201)..(1346)

<400> 116
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aacttttacg aggtatcagc acttttcttt cattaggggg aaggcgtgag gaaagtacca 60

aacagcagcg gagttttaaa ctttaaatag acaggtctga gtgcctgaac ttgccttttc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233
                      Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu
                       1               5                  10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca     281
Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser
```

207

```
gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca    329
Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser
         30              35                  40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct    377
Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro
         45              50                  55

ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg    425
Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val
60              65                  70                      75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg    473
Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu
             80                  85                  90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac    521
Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn
             95                  100                 105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg    569
Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val
         110                 115                 120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att    617
Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile
         125                 130                 135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac    665
Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr
140                 145                 150                 155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg    713
Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu
             160                 165                 170

atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc    761
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys
             175                 180                 185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc    809
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro
         190                 195                 200

acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg    857
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val
         205                 210                 215

tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc    905
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly
220                 225                 230                 235

gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt    953
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser
             240                 245                 250
```

208

```
ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat   1001
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr
            255             260             265

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct   1049
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro
            270             275             280

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc   1097
Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg
        285             290             295

aat tac aac aag caa gca agt gag caa aac tgg gct aat tac agt gca   1145
Asn Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala
300             305             310             315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat   1193
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His
            320             325             330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta   1241
Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu
            335             340             345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct   1289
Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro
        350             355             360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac   1337
Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp
        365             370             375

ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt          1386
Leu Glu Ile
380

ggagaagaaa aaaggtgctg tagaaagtgc accaggtgtt aattttgatc cggtggaggt 1446

ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506

tcactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg 1566

gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626

catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686

gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg 1746

ccaggaataa atacttcctg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806

gtccttaagt ccctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt 1866

ctaggcctga ccctccaggt gtcaatggac ttgtgctact atattttttt attcttggta 1926

tcagtttaaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986
```

209

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   atattctttt tccatccact tgcacaatat cattaccatc acttttttcat cattcctcag 2046

   ctactactca cattcattta atggtttctg taaacatttt taagacagtt gggatgtcac 2106

   ttaacatttt tttttttgagc taaagtcagg gaatcaagcc atgcttaata tttaacaatc 2166

   acttatatgt gtgtcgaaga gtttgttttg tttgtcatgt attggtacaa gcagatacag 2226

   tataaactca caaacacaga tttgaaaata atgcacatat ggtgttcaaa tttgaacctt 2286

   tctcatggat ttttgtggtg tgggccaata tggtgtttac attatataat tcctgctgtg 2346

   gcaagtaaag cacacttttt ttttctccta aaatgttttt ccctgtgtat cctattatgg 2406

   atactggttt tgttaattat gattctttat tttctctcct tttttttagga tatagcagta 2466

   atgctattac tgaaatgaat ttcctttttc tgaaatgtaa tcattgatgc ttgaatgata 2526

   gaatttttagt actgtaaaca ggctttagtc attaatgtga gagacttaga aaaaaatgct 2586

   tagagtggac tattaaatgt gcctaaatga attttgcagt aactggtatt cttgggtttt 2646

   cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtcttttgg 2706

   agtgaccagc aactttgatg tttgcactaa gatttttattt ggaatgcaag agaggttgaa 2766

   agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826

   cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

   tgacactttt cttcttgcat gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

   ctaatttgtt tgacattcca tgttaaacta cggtcatgtt cagcttcatt gcatgtaatg 3006

   tagacctagt ccatcagatc atgtgttctg gagagtgttc tttattcaat aaagttttaa 3066

   tttagtat                                                         3074


<210> 117
<211> 398
<212> PRT
<213> Homo sapiens

<400> 117
Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met
 1               5                  10                  15

Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu Glu Ala Gly Ala
            20                  25                  30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
        35                  40                  45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
    50                  55                  60
```

210

```
-Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
 65               70                  75                  80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly
                 85                  90                  95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg
                100             105             110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
            115             120             125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe
    130             135              ,140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
145             150             155             160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
                165             170             175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
            180             185             190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
    195             200             205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
    210             215             220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
225             230             235             240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
                245             250             255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
    260             265             270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
    275             280             285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
    290             295             300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
305             310             315             320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
                325             330             335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
            340             345             350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
    355             360             365
```

```
Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
    370             375         380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
385             390             395
```

<210> 118
<211> 2054
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (76)..(1269)

<400> 118

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cacacagctc agaacagctg gatcttgctc agtctctgcc aggggaagat tccttggagg   60

aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc   111
               Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu
                 1               5                   10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag   159
Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu
         15              20                  25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act   207
Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr
     30                  35                  40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg   255
Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met
 45                  50                  55                  60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag   303
Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys
                 65                  70                  75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag   351
Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu
             80                  85                  90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca   399
Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala
             95                  100                 105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg   447
Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
     110                 115                 120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt   495
Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
125             130                 135                 140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga   543
Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
```

```
agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc   591
Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr
        160             165             170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc   639
Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile
        175             180             185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc   687
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser
        190             195             200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg   735
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu
205             210             215             220

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca   783
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr
        225             230             235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag   831
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys
        240             245             250

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta   879
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu
        255             260             265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt   927
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg
        270             275             280

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca   975
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser
285             290             295             300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa   1023
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu
        305             310             315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga   1071
Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly
        320             325             330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat   1119
Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp
        335             340             345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag   1167
Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys
        350             355             360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag   1215
Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu
365             370             375             380
```

213

```
aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa    1263
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln
            385                 390                 395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca    1319
Glu Leu

ggacaaaatg caaacttttt tttttctga dacagagtct tgctctgtcg ccaagttgca    1379

gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa    1439

aaaaaaaaaa aaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc    1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt    1559

tggatacagg agaagaaaca gcggctccac tacagaccca gccccaggtt caatgtcctc    1619

cgaagaatga agtctttccc tggtgatggt cccctgccct gtctttccag catccactct    1679

cccttgtcct cctgggggca tatctcagtc aggcagcggc ttcctgatga tggtcgttgg    1739

ggtggttgtc atgtgatggg tcccctccag gttactaaag ggtgcatgtc ccctgcttga    1799

acactgaagg gcaggtggtg agccatggcc atggtcccca gctgaggagc aggtgtccct    1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct    1919

cttacccggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa    1979

gctcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa    2039

actcacctac tcatc                                                    2054


<210> 119
<211> 398
<212> PRT
<213> Homo sapiens

<400> 119
Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met
  1               5                  10                  15

Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly Ala
            20                  25                  30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
        35                  40                  45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
    50                  55                  60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
65                  70                  75                  80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly
```

214

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg
        100   105   110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
        115   120   125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe
        130   135   140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
145   150   155   160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
        165   170   175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
        180   185   190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
        195   200   205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
210   215   220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
225   230   235   240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
        245   250   255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
        260   265   270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
        275   280   285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
        290   295   300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
305   310   315   320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
        325   330   335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
        340   345   350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
        355   360   365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
        370   375   380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu

215

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<210> 120
<211> 2054
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (76)..(1269)

<400> 120
cacacagctc agaacagctg gatcttgctc agtctctgcc aggggaagat tccttggagg 60

aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc    111
               Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu
                1                 5                    10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg aga gtg agg gca gag    159
Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu
         15                  20                  25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act    207
Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr
     30                  35                  40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg    255
Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met
 45                  50                  55                  60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag    303
Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys
                 65                  70                  75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag    351
Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu
             80                  85                  90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca    399
Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala
         95                  100                 105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg    447
Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
     110                 115                 120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt    495
Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
125                 130                 135                 140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga    543
Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
                 145                 150                 155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc    591
Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr
```

```
acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc   639
Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile
        175             180             185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc   687
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser
        190             195             200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg   735
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu
205             210             215             220

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca   783
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr
        225             230             235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag   831
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys
        240             245             250

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta   879
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu
        255             260             265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt   927
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg
        270             275             280

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca   975
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser
285             290             295             300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa  1023
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu
        305             310             315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga  1071
Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly
        320             325             330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat  1119
Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp
        335             340             345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag  1167
Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys
        350             355             360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag  1215
Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu
365             370             375             380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa  1263
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln
        385             390             395
```

217

```
gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca      1319
Glu Leu

ggacaaaatg caaacttttt tttttctga gacagagtct tgctctgtcg ccaagttgca      1379

gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa      1439

aaaaaaaaaa aaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc      1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt      1559

tggatacagg agaagaaaca gcggctccac tacagaccca gccccaggtt caatgtcctc      1619

cgaagaatga agtctttccc tggtgatggt ccctgccct gtctttccag catccactct      1679

cccttgtcct cctggggggca tatctcagtc aggcagcggc ttcctgatga tggtcgttgg      1739

ggtggttgtc atgtgatggg tcccctccag gttactaaag ggtgcatgtc ccctgcttga      1799

acactgaagg gcaggtggtg agccatggcc atggtcccca gctgaggagc aggtgtccct      1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct      1919

cttacccggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa      1979

gctcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa      2039

actcacctac tcatc                                                     2054


<210> 121
<211> 108
<212> PRT
<213> Homo sapiens

<400> 121
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1               5                   10                  15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
            20                  25                  30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
        35                  40                  45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
    50                  55                  60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65                  70                  75                  80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
                85                  90                  95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
            100                 105
```

218

<210> 122
<211> 1546
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (89)..(412)

<400> 122
actaggcaga gccgtggaac cgccgccagg tcgctgttgg tccacgccgc cgtcgcgcc 60

gcccgcccgc tcagcgtccg ccgccgcc atg gga gtg cag gtg gaa acc atc   112
                                 Met Gly Val Gln Val Glu Thr Ile
                                  1   5

tcc cca gga gac ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg   160
Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val
     10   15   20

gtg cac tac acc ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc   208
Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser
 25   30   35   40

cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg   256
Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val
                 45   50   55

atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga   304
Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg
             60   65   70

gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac   352
Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His
             75   80   85

cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt   400
Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
     90   95   100

cta aaa ctg gaa tgacaggaat ggcctcctcc cttagctccc tgttcttgga   452
Leu Lys Leu Glu
105

tctgccatgg agggatctgg tgcctccaga catgtgcaca tgaatccata tggagctttt 512

cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc 572

agctttgctt ccgacacctc tgtttcctct tccccttct cctcgtatgt gtgtttacct 632

aaactatatg ccataaacct caagttactc attttatttt gttttcattt tggggtgaag 692

attcagtttc agtcttttgg atataggttt ccaattaagt acatggtcaa gtattaacag 752

cacaagtggt aggttaacat tagaatagga attggtgttg gggggggggt ttgcaagaat 812

219

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attttatttt aattttttgg atgaaatttt tatctattat atattaaaca ttcttgctgc 872

tgcgctgcaa agccatagca gatttgaggc gctgttgagg actgaattac tctccaagtt 932

gagagatgtc tttgggttaa attaaaagcc ctacctaaaa ctgaggtggg gatggggaga 992

gcctttgcct ccaccattcc cacccaccct cccctttaaac cctctgcctt tgaaagtaga 1052

tcatgttcac tgcaatgctg gacactacag gtatctgtcc ctgggccagc agggacctct 1112

gaagccttct ttgtggcctt tttttttttt tcatcctgtg gtttttctaa tggactttca 1172

ggaattttgt aatctcataa cttttccaagc tccaccactt cctaaatctt aagaacttta 1232

attgacagtt tcaattgaag gtgctgtttg tagacttaac acccagtgaa agcccagcca 1292

tcatgacaaa tccttgaatg ttctcttaag aaaatgatgc tggtcatcgc agcttcagca 1352

tctcctgttt tttgatgctt ggctccctct gctgatctca gtttcctggc ttttcctccc 1412

tcagcccctt ctcaccccctt tgctgtcctg tgtagtgatt tggtgagaaa tcgttgctgc 1472

accttcccc cagcaccatt tatgagtctc aagttttatt attgcaataa aagtgcttta 1532

tgccggcttt tctc                                                   1546


<210> 123
<211> 679
<212> PRT
<213> Homo sapiens

<400> 123
Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala Thr Ala Ala Ser Gly
 1               5                  10                  15

Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu Gly Phe Ile Ile Ala
            20                  25                  30

Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp Val Ala Asn Ser Phe
         35                  40                  45

Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu Lys Gln Ala Cys Ile
      50                  55                  60

Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val Leu Leu Gly Ala Lys
 65                  70                  75                  80

Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp Val Glu Met Tyr Asn
                 85                  90                  95

Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val Ser Ala Met Phe Gly
            100                 105                 110

Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile Ser
         115                 120                 125
```

220

```
Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe Ser Leu Val Ala
    130             135             140

Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu Ile Lys Ile Val Met
145             150             155             160

Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met Ser Gly Ile Leu
            165             170             175

Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys Ala Asp Pro Val Pro
            180             185             190

Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala Cys Thr Val Gly Ile
            195             200             205

Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe Asp
    210             215             220

Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala Val
225             230             235             240

Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys Arg
            245             250             255

Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser Glu Ser Pro Leu Met
            260             265             270

Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu Glu Thr Lys Leu Ser
            275             280             285

Val Gly Asp Ile Glu Asn Lys His Pro Val Ser Glu Val Gly Pro Ala
    290             295             300

Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys
305             310             315             320

Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Ser Val
            325             330             335

Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Val Asn Gly Ala Val
            340             345             350

Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Ala Val Ser Asn
            355             360             365

Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp
    370             375             380

Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val
385             390             395             400

Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn
            405             410             415

Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser
            420             425             430
```

221

```
Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu Glu Met Glu Lys Leu
        435             440             445

Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile Arg Met Asp Ser Tyr
        450             455             460

Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Ala Ser Glu Ile
465             470             475             480

Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser
            485             490             495

Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser
        500             505             510

Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe
        515             520             525

Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala
        530             535             540

Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser Ser Lys Val Ala Thr
545             550             555             560

Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Val Gly Leu
            565             570             575

Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr
        580             585             590

Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu
        595             600             605

Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His
        610             615             620

Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys
625             630             635             640

Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val
            645             650             655

Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Ile Phe
            660             665             670

Arg Tyr Val Ile Leu Arg Met
        675


<210> 124
<211> 2916
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
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<400> 124

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aacaaccact actccagaga atg gca acg ctg att acc agt act aca gct gct 113
                        Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala
                         1   5   10

acc gcc gct tct ggt cct ttg gtg gac tac cta tgg atg ctc atc ctg   161
Thr Ala Ala Ser Gly Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu
             15   20   25

ggc ttc att att gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat   209
Gly Phe Ile Ile Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp
         30   35   40

gta gca aat tct ttt ggt aca gct gtg ggc tca ggt gta gtg acc ctg   257
Val Ala Asn Ser Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu
     45   50   55

aag caa gcc tgc atc cta gct agc atc ttt gaa aca gtg ggc tct gtc   305
Lys Gln Ala Cys Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val
 60   65   70   75

tta ctg ggg gcc aaa gtg agc gaa acc atc cgg aag ggc ttg att gac   353
Leu Leu Gly Ala Lys Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp
             80   85   90

gtg gag atg tac aac tcg act caa ggg ctg ctg atg gcc ggc tca gtc   401
Val Glu Met Tyr Asn Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val
             95   100   105

agt gct atg ttt ggt tct gct gtg tgg caa ctc gtg gct tcg ttt ttg   449
Ser Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu
         110   115   120

aag ctc cct att tct gga acc cat tgt att gtt ggt gca act att ggt   497
Lys Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly
     125   130   135

ttc tcc ctc gtg gca aag ggg cag gag ggt gtc aag tgg tct gaa ctg   545
Phe Ser Leu Val Ala Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu
140   145   150   155

ata aaa att gtg atg tct tgg ttc gtg tcc cca ctg ctt tct gga att   593
Ile Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile
                 160   165   170

atg tct gga att tta ttc ttc ctg gtt cgt gca ttc atc ctc cat aag   641
Met Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys
             175   180   185

gca gat cca gtt cct aat ggt ttg cga gct ttg cca gtt ttc tat gcc   689
Ala Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala
         190   195   200

223

```
tgc aca gtt gga ata aac ctc ttt tcc atc atg tat act gga gca ccg   737
Cys Thr Val Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro
    205                 210                 215

ttg ctg ggc ttt gac aaa ctt cct ctg tgg ggt acc atc ctc atc tcg   785
Leu Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser
220                 225                 230                 235

gtg gga tgt gca gtt ttc tgt gcc ctt atc gtc tgg ttc ttt gta tgt   833
Val Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys
                240                 245                 250

ccc agg atg aag aga aaa att gaa cga gaa ata aag tgt agt cct tct   881
Pro Arg Met Lys Arg Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser
                255                 260                 265

gaa agc ccc tta atg gaa aaa aag aat agc ttg aaa gaa gac cat gaa   929
Glu Ser Pro Leu Met Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu
            270                 275                 280

gaa aca aag ttg tct gtt ggt gat att gaa aac aag cat cct gtt tct   977
Glu Thr Lys Leu Ser Val Gly Asp Ile Glu Asn Lys His Pro Val Ser
    285                 290                 295

gag gta ggg cct gcc act gtg ccc ctc cag gct gtg gtg gag gag aga   1025
Glu Val Gly Pro Ala Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg
300                 305                 310                 315

aca gtc tca ttc aaa ctt gga gat ttg gag gaa gct cca gag aga gag   1073
Thr Val Ser Phe Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu
                320                 325                 330

agg ctt ccc agc gtg gac ttg aaa gag gaa acc agc ata gat agc acc   1121
Arg Leu Pro Ser Val Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr
                335                 340                 345

gtg aat ggt gca gtg cag ttg cct aat ggg aac ctt gtc cag ttc agt   1169
Val Asn Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser
            350                 355                 360

caa gcc gtc agc aac caa ata aac tcc agt ggc cac tac cag tat cac   1217
Gln Ala Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His
    365                 370                 375

acc gtg cat aag gat tcc ggc ctg tac aaa gag cta ctc cat aaa tta   1265
Thr Val His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu
380                 385                 390                 395

cat ctt gcc aag gtg gga gat tgc atg gga gac tcc ggt gac aaa ccc   1313
His Leu Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro
                400                 405                 410

tta agg cgc aat aat agc tat act tcc tat acc atg gca ata tgt ggc   1361
Leu Arg Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly
                415                 420                 425

atg cct ctg gat tca ttc cgt gcc aaa gaa ggt gaa cag aag ggc gaa   1409
```

```
    Met Pro Leu Asp Ser Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu
            430                 435                 440

gaa atg gag aag ctg aca tgg cct aat gca gac tcc aag aag cga att    1457
Glu Met Glu Lys Leu Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile
    445                 450                 455

cga atg gac agt tac acc agt tac tgc aat gct gtg tct gac ctt cac    1505
Arg Met Asp Ser Tyr Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His
460                 465                 470                 475

tca gca tct gag ata gac atg agt gtc aag gca gag atg ggt cta ggt    1553
Ser Ala Ser Glu Ile Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly
                480                 485                 490

gac aga aaa gga agt aat ggc tct cta gaa gaa tgg tat gac cag gat    1601
Asp Arg Lys Gly Ser Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp
            495                 500                 505

aag cct gaa gtc tct ctc ctc ttc cag ttc ctg cag atc ctt aca gcc    1649
Lys Pro Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala
            510                 515                 520

tgc ttt ggg tca ttc gcc cat ggt ggc aat gac gta agc aat gcc att    1697
Cys Phe Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile
            525                 530                 535

ggg cct ctg gtt gct tta tat ttg gtt tat gac aca gga gat gtt tct    1745
Gly Pro Leu Val Ala Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser
540                 545                 550                 555

tca aaa gtg gca aca cca ata tgg ctt cta ctc tat ggt ggt gtt ggt    1793
Ser Lys Val Ala Thr Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly
                560                 565                 570

atc tgt gtt ggt ctg tgg gtt tgg gga aga aga gtt atc cag acc atg    1841
Ile Cys Val Gly Leu Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met
            575                 580                 585

ggg aag gat ctg aca ccg atc aca ccc tct agt ggc ttc agt att gaa    1889
Gly Lys Asp Leu Thr Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu
            590                 595                 600

ctg gca tct gcc ctc act gtg gtg att gca tca aat att ggc ctt ccc    1937
Leu Ala Ser Ala Leu Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro
            605                 610                 615

atc agt aca aca cat tgt aaa gtg ggc tct gtt gtg tct gtt ggc tgg    1985
Ile Ser Thr Thr His Cys Lys Val Gly Ser Val Val Ser Val Gly Trp
620                 625                 630                 635

ctc cgg tcc aag aag gct gtt gac tgg cgt ctc ttt cgt aac att ttt    2033
Leu Arg Ser Lys Lys Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe
                640                 645                 650

atg gcc tgg ttt gtc aca gtc cct att tct gga gtt atc agt gct gcc    2081
Met Ala Trp Phe Val Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala
```

```
atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctgtt        2127
Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met
        670             675

tgagattaaa atttgtgtca atgtttggga ccatcttagg tattcctgct cccctgaaga 2187

atgattacag tgttaacaga agactgacaa gagtcttttt atttgggagc cagaggaggg 2247

aagtgttact tgtgctataa ctgcttttgt gctaaatatg aattgtctca aaattagctg 2307

tgtaaaatag cccgggttcc actggctcct gctgaggtcc cctttccttc tgggctgtga 2367

attcctgtac atatttctct actttttgta tcaggcttca attccattat gttttaatgt 2427

tgtctctgaa gatgacttgt gatttttttt tctttttttt aaaccatgaa gagccgtttg 2487

acagagcatg ctctgcgttg ttggtttcac cagcttctgc cctcacatgc acagggattt 2547

aacaacaaaa atataactac aacttccctt gtagtctctt atataagtag agtccttggt 2607

actctgccct cctgtcagta gtggcaggat ctattggcat attcgggagc ttcttagagg 2667

gatgaggttc tttgaacaca gtgaaaattt aaattagtaa cttttttgca agcagtttat 2727

tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gttggcaatc ttggttattt 2787

ctttaagatt tctggcagtg tgggatggat gaatgaagtg gaatgtgaac tttgggcaag 2847

ttaaatggga cagccttcca tgttcatttg tctacctctt aactgaataa aaaagcctac 2907

agtttttag                                                       2916
```

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<210> 125
<211> 288
<212> PRT
<213> Homo sapiens

<400> 125
Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln Asp Leu Ser Glu Ala
 1               5                   10                  15

Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu
            20                  25                  30

Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys
        35                  40                  45

Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu
    50                  55                  60

Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro
65                  70                  75                  80

Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp
```

226

Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln
        100   105   110

Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu
        115   120   125

Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly
        130   135   140

Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser
145   150   155   160

Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr
                165   170   175

Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr
                180   185   190

Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu
                195   200   205

Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp
        210   215   220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala
225   230   235   240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys
                245   250   255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu
                260   265   270

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met
        275   280   285

<210> 126
<211> 1550
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (81)..(944)

<400> 126
tcaacgcctg cctcccctcg agcgtcctca gcgcagccgc cgcccgcgga gccagcacga   60

acgagcccag caccggccgg atg gag cgt ccg caa ccc gac agc atg ccc cag   113
                       Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln
                        1   5   10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag   161
Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln

```
gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc    209
Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr
         30                  35                  40

cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg    257
Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val
         45                  50                  55

gcc ctg gag gag gag att gag cgc aac aag gag agc cca gtc ttc gcc    305
Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala
60                  65                  70                  75

cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag    353
Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln
                 80                  85                  90

gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac    401
Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr
             95                 100                 105

aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtg ggg cgc    449
Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg
            110                 115                 120

aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt    497
Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly
        125                 130                 135

gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg    545
Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu
140                 145                 150                 155

gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac    593
Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn
                160                 165                 170

att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac    641
Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn
            175                 180                 185

tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc    689
Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala
        190                 195                 200

aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag    737
Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu
        205                 210                 215

ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg    785
Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly
220                 225                 230                 235

ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag    833
Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu
            240                 245                 250
```

228

```
act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt   881
Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu
            255                 260                 265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta   929
Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val
        270                 275                 280

ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt   984
Gly Leu Tyr Ala Met
    285

ccggtggaag gccttctttc tagagaggga attctcttgg ctggcttcct taccgtgggc 1044

actgaaggct ttcagggcct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa 1104

ggagcctatg gcatcttccc caacgaaaag cacatccagg caatggccta aacttcagag 1164

ggggcgaagg ggtcagccct gcccttcagc atcctcagtt cctgcagcag agcctggaag 1224

acaccctaat gtggcagctg tctcaaacct ccaaaagccc tgagtttcaa gtatccttgt 1284

tgacacggcc atgaccactt tccccgtggg ccatggcaat ttttacacaa acctgaaaag 1344

atgttgtgtc ttgtgttttt gtcttatttt tgttggagcc actctgttcc tggctcagcc 1404

tcaaatgcag tattttttgtt gtgttctgtt gtttttatag cagggttggg gtggttttg 1464

agccatgcgt gggtggggag ggaggtgttt aacggcactg tggccttggt ctaactttg 1524

tgtgaaataa taaacaacat tgtctg                                      1550


<210> 127
<211> 135
<212> PRT
<213> Homo sapiens

<400> 127
Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu
 1               5                  10                  15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val
            20                  25                  30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro
         35                  40                  45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys
     50                  55                  60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe
 65                  70                  75                  80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn
                85                  90                  95
```

229

```
      Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg
              100                 105                 110

      Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys
              115                 120                 125

      Ile Lys Cys Val Ala Phe Asp
          130                 135


      <210> 128
      <211> 507
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (50)..(454)

      <400> 128
      cttctgacag ctggtgcgcc tgcccgggaa catcctcctg gactcaatc atg gct tgt 58
                                                               Met Ala Cys
                                                                 1

      ggt ctg gtc gcc agc aac ctg aat ctc aaa cct gga gag tgc ctt cga   106
      Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg
          5                   10                  15

      gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg   154
      Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu
       20                  25                  30                  35

      ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac   202
      Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn
                      40                  45                  50

      gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggg   250
      Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly
                  55                  60                  65

      gcc tgg ggg acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga   298
      Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly
              70                  75                  80

      agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc   346
      Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val
          85                  90                  95

      aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg   394
      Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu
      100                 105                 110                 115

      gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt   442
      Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys
                      120                 125                 130
```

230

```
gtg gcc_ttt_gac tgaaatcagc cagcccatgg cccccaataa aggcagctgc      -  494-
Val Ala Phe Asp
            135

ctctgctccc ctg                                                     507


<210> 129
<211> 662
<212> PRT
<213> Homo sapiens

<400> 129
Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn
 1               5                  10                  15

Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn
                20                  25                  30

Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp
            35                  40                  45

Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys
        50                  55                  60

Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser
 65                  70                  75                  80

Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr
                85                  90                  95

Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu
            100                 105                 110

Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys
            115                 120                 125

His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile
            130                 135                 140

Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu
145                 150                 155                 160

Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro
                165                 170                 175

Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg
                180                 185                 190

Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr
            195                 200                 205

Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu
        210                 215                 220

Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu
225                 230                 235                 240
```

231

Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu
            245   250   255

Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr
            260   265   270

Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln
            275   280   285

Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys
            290   295   300

Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val
305   310   315   320

Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala
            325   330   335

Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe
            340   345   350

Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp
            355   360   365

Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln
            370   375   380

Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp
385   390   395   400

Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu
            405   410   415

Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe
            420   425   430

Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn
            435   440   445

Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile
            450   455   460

Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp
465   470   475   480

Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu
            485   490   495

Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser
            500   505   510

Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr
            515   520   525

Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn
            530   535   540

232

```
Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly
545             550             555             560

Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln
                565             570             575

Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln
            580             585             590

Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn
        595             600             605

Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe
        610             615             620

Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn
625             630             635             640

Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg
                645             650             655

Leu Arg Ile Ser Glu Lys
            660
```

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<210> 130
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<212> DNA
<213> Homo sapiens

<220>
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<222> (74)..(2059)

<400> 130
cttggctgga cagtttgtga aactgtgttg ccgggcaact ggacatcctt ttgttcaata   60

tcagtggttc aaa atg aat aaa gag att cca aat gga aat aca tca gag      109
            Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu
            1               5                   10

ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt   157
Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys
        15                  20                  25

cga gtt aat aac aat ttc acc ttt gaa ttc agc cag tgg tca cag ctg   205
Arg Val Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu
    30              35                  40

gat gtt tgc gac atc cca gag agc ttc cag aga agt gtt gat ggc gtc   253
Asp Val Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val
45              50                  55                  60

tct gaa tcc aag ttg caa atc tgt gtt gaa cca act tcc caa aag ctg   301
Ser Glu Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu
            65                  70                  75
```

233

```
atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct      349
Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro
            80                      85                  90

att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag      397
Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu
            95                     100             105

acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga      445
Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly
            110                    115             120

acc tac tgg tgt cat gta tat aat gat cga gac agt caa gat agc aag      493
Thr Tyr Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys
125                     130             135                 140

aag gta gaa atc atc ata gga aga aca gat gag gca gtg gag tgc act      541
Lys Val Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr
                145                    150             155

gaa gat gaa tta aat aat ctt ggt cat cct gat aat aaa gag caa aca      589
Glu Asp Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr
                160                    165             170

act gac cag cct ttg gcg aag gac aag gtt gcc ctt ttg ata gga aat      637
Thr Asp Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn
            175                    180             185

atg aat tac cgg gag cac ccc aag ctc aaa gct cct ttg gtg gat gtg      685
Met Asn Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val
            190                    195             200

tac gaa ttg act aac tta ctg aga cag ctg gac ttc aaa gtg gtt tca      733
Tyr Glu Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser
205                     210             215                 220

ctg ttg gat ctt act gaa tat gag atg cgt aat gct gtg gat gag ttt      781
Leu Leu Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe
                225                    230             235

tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga      829
Leu Leu Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly
            240                    245             250

cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct      877
His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala
            255                    260             265

cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg      925
Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu
            270                    275             280

aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat      973
Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp
285                     290             295                 300
```

234

```
atg tgt agg aaa aga aat gac tac gat gat acc att cca atc ttg gat   1021
Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp
            305             310                 315

gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa   1069
Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln
            320             325             330

gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc   1117
Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile
            335             340             345

ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act   1165
Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr
            350             355             360

gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc   1213
Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr
365             370             375             380

aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga   1261
Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg
            385             390             395

gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt   1309
Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu
            400             405             410

gtg cgg aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg   1357
Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met
            415             420             425

tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct   1405
Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala
            430             435             440

gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca   1453
Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro
445             450             455             460

ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat   1501
Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp
            465             470             475

cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act   1549
Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr
            480             485             490

ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc   1597
Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr
            495             500             505

aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta   1645
Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val
510             515             520

tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag   1693
```

235

```
Cys Leu Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys
525             530             535             540
```

```
cag gaa gtg aat gtt ggg aaa cct ctc att gct aaa tta gac atg cat   1741
Gln Glu Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His
                545             550             555
```

```
cga ggt ttg gga agg aag act tgc ttt caa act tgt ctt atg tct aat   1789
Arg Gly Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn
                560             565             570
```

```
ggt cct tac cag agt tct gca gcc acc tca gga gga gca ggg cat tat   1837
Gly Pro Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr
            575             580             585
```

```
cac tca ttg caa gac cca ttc cat ggt gtt tac cat tca cat cct ggt   1885
His Ser Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly
    590             595             600
```

```
aat cca agt aat gtt aca cca gca gat agc tgt cat tgc agc cgg act   1933
Asn Pro Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr
605             610             615             620
```

```
cca gat gca ttt att tca agt ttc gct cac cat gct tca tgt cat ttt   1981
Pro Asp Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe
            625             630             635
```

```
agt aga agt aat gtg cca gta gag aca act gat gaa ata cca ttt agt   2029
Ser Arg Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser
            640             645             650
```

```
ttc tct gac agg ctc aga att tct gaa aaa tgacctcctt gttttgaaa      2079
Phe Ser Asp Arg Leu Arg Ile Ser Glu Lys
            655             660
```

```
gttagcataa ttttagatgc ctgtgaaata gtactgcact tacataaagt gagacattgt 2139
```

```
gaaaaggcaa atttgtatat gtagagaaag aatagtagta actgtttcat agcaaacttc 2199
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```
aggactttga gatgttgaaa ttacattatt taattacaga cttcctcttt ct         2251
```


<210> 131
<211> 824
<212> PRT
<213> Homo sapiens

<400> 131
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Met Ser Leu Leu Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala
 1               5               10              15
```

```
Pro Thr Gly Pro Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg
            20              25              30
```

```
Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala
        35              40              45
```

236

-Pro-Glu-Gly-Arg-Gly-Trp-Arg-Arg-Leu-Ala-Glu-Leu-Ala-Gly-Ser-Arg-
     50   55   60

Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys
65   70   75   80

Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met
             85   90   95

Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala
         100   105   110

Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys
         115   120   125

Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val
     130   135   140

Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp
145   150   155   160

Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile
             165   170   175

Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val
             180   185   190

Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val
         195   200   205

Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu
     210   215   220

Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro
225   230   235   240

Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro
             245   250   255

His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys
         260   265   270

Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr
     275   280   285

Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val
     290   295   300

Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp
305   310   315   320

Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp
             325   330   335

Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn
     340   345   350

237

─────Tyr─Arg─Glu─His─Pro─Lys─Leu─Lys─Ala─Pro─Leu─Val─Asp─Val─Tyr─Glu─────────────
        355   360   365

Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu
    370   375   380

Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu
385   390   395   400

Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly
          405   410   415

Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn
        420   425   430

Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu
        435   440   445

Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys
    450   455   460

Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu
465   470   475   480

Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala
        485   490   495

Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met
        500   505   510

Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu
        515   520   525

Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly
    530   535   540

Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu
545   550   555   560

Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg
        565   570   575

Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu
        580   585   590

Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe
        595   600   605

Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu
    610   615   620

Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp
625   630   635   640

Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser
        645   650   655

```
-Tyr Leu Val-Ser Lys-Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu
            660             665             670

Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu
        675             680             685

Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu
    690             695             700

Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly
705             710             715             720

Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro
            725             730             735

Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser
        740             745             750

Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro
        755             760             765

Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp
    770             775             780

Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg
785             790             795             800

Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser
            805             810             815

Asp Arg Leu Arg Ile Ser Glu Lys
            820


<210> 132
<211> 2828
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (165)..(2636)

<400> 132
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gcccctgcct ccgcggctcg gaggcgagcg gaaggtgccc cggggccgag gcccgtgacg  120

gggcgggcgg gagccccggc agtccggggt cgccggcgag ggcc atg tcg ctg ttg  176
                                             Met Ser Leu Leu
                                              1

ggg gac ccg cta cag gcc ctg ccg ccc tcg gcc gcc ccc acg ggg ccg  224
Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala Pro Thr Gly Pro
  5                10                15                20

ctg ctc gcc cct ccg gcc ggc gcg acc ctc aac cgc ctg cgg gag ccg  272
```

239

```
ctg ctg cgg agg ctc agc gag ctc ctg gat cag gcg ccc gag ggc cgg    320
Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala Pro Glu Gly Arg
            40                  45                  50

ggc tgg agg aga ctg gcg gag ctg gcg ggg agt cgc ggg cgc ctc cgc    368
Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg Gly Arg Leu Arg
            55                  60                  65

ctc agt tgc cta gac ctg gag cag tgt tct ctt aag gta ctg gag cct    416
Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys Val Leu Glu Pro
        70                  75                  80

gaa gga agc ccc agc ctg tgt ctg ctg aag tta atg ggt gaa aaa ggt    464
Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met Gly Glu Lys Gly
85                  90                  95                  100

tgc aca gtc aca gaa ttg agt gat ttc ctg cag gct atg gaa cac act    512
Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala Met Glu His Thr
                105                 110                 115

gaa gtt ctt cag ctt ctc agc ccc cca gga ata aag att act gta aac    560
Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys Ile Thr Val Asn
                120                 125                 130

cca gag tca aag gca gtc ttg gct gga cag ttt gtg aaa ctg tgt tgc    608
Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val Lys Leu Cys Cys
            135                 140                 145

cgg gca act gga cat cct ttt gtt caa tat cag tgg ttc aaa atg aat    656
Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp Phe Lys Met Asn
        150                 155                 160

aaa gag att cca aat gga aat aca tca gag ctt att ttt aat gca gtg    704
Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn Ala Val
165                 170                 175                 180

cat gta aaa gat gca ggc ttt tat gtc tgt cga gtt aat aac aat ttc    752
His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn Asn Phe
                185                 190                 195

acc ttt gaa ttc agc cag tgg tca cag ctg gat gtt tgc gac atc cca    800
Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp Ile Pro
                200                 205                 210

gag agc ttc cag aga agt gtt gat ggc gtc tct gaa tcc aag ttg caa    848
Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys Leu Gln
            215                 220                 225

atc tgt gtt gaa cca act tcc caa aag ctg atg cca ggc agc aca ttg    896
Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser Thr Leu
        230                 235                 240

gtt tta cag tgt gtt gct gtt gga agc cct att cct cac tac cag tgg    944
Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr Gln Trp
```

240

```
ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg    992
Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met
            265             270             275

gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta   1040
Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val
            280             285             290

tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata   1088
Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile
            295             300             305

gga aga aca gat gag gca gtg gag tgc act gaa gat gaa tta aat aat   1136
Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu Asn Asn
            310             315             320

ctt ggt cat cct gat aat aaa gag caa aca act gac cag cct ttg gcg   1184
Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro Leu Ala
325             330             335             340

aag gac aag gtt gcc ctt ttg ata gga aat atg aat tac cgg gag cac   1232
Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg Glu His
            345             350             355

ccc aag ctc aaa gct cct ttg gtg gat gtg tac gaa ttg act aac tta   1280
Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr Asn Leu
            360             365             370

ctg aga cag ctg gac ttc aaa gtg gtt tca ctg ttg gat ctt act gaa   1328
Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu Thr Glu
            375             380             385

tat gag atg cgt aat gct gtg gat gag ttt tta ctc ctt tta gac aag   1376
Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu Asp Lys
            390             395             400

gga gta tat ggg tta tta tat tat gca gga cat ggt tat gaa aat ttt   1424
Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu Asn Phe
405             410             415             420

ggg aac agc ttc atg gtc ccc gtt gat gct cca aat cca tat agg tct   1472
Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr Arg Ser
            425             430             435

gaa aat tgt ctg tgt gta caa aat ata ctg aaa ttg atg caa gaa aaa   1520
Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln Glu Lys
            440             445             450

gaa act gga ctt aat gtg ttc tta ttg gat atg tgt agg aaa aga aat   1568
Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys Arg Asn
            455             460             465

gac tac gat gat acc att cca atc ttg gat gca cta aaa gtc acc gcc   1616
Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val Thr Ala
470             475             480
```

241

```
aat att gtg ttt gga tat gcc acg tgt caa gga gca gaa gct ttt gaa    1664
Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala Phe Glu
485                 490                 495                 500

atc cag cat tct gga ttg gca aat gga atc ttt atg aaa ttt tta aaa    1712
Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe Leu Lys
                505                 510                 515

gac aga tta tta gaa gat aag aaa atc act gtg tta ctg gat gaa gtt    1760
Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp Glu Val
                520                 525                 530

gca gaa gat atg ggt aag tgt cac ctt acc aaa ggc aaa cag gct cta    1808
Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln Ala Leu
                535                 540                 545

gag att cga agt agt tta tct gag aag aga gca ctt act gat cca ata    1856
Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp Pro Ile
        550                 555                 560

cag gga aca gaa tat tct gct gaa tct ctt gtg cgg aat cta cag tgg    1904
Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu Gln Trp
565                 570                 575                 580

gcc aag gct cat gaa ctt cca gaa agt atg tgt ctt aag ttt gac tgt    1952
Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe Asp Cys
                585                 590                 595

ggt gtt cag att caa tta gga ttt gca gct gag ttt tcc aat gtc atg    2000
Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn Val Met
                600                 605                 610

atc atc tat aca agt ata gtt tac aaa cca ccg gag ata ata atg tgt    2048
Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile Met Cys
        615                 620                 625

gat gcc tac gtt act gat ttt cca ctt gat cta gat att gat cca aaa    2096
Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp Pro Lys
        630                 635                 640

gat gca aat aaa ggc aca cct gaa gaa act ggc agc tac ttg gta tca    2144
Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu Val Ser
645                 650                 655                 660

aag gat ctt ccc aag cat tgc ctc tat acc aga ctc agt tca ctg caa    2192
Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser Leu Gln
                665                 670                 675

aaa tta aag gaa cat cta gtc ttc aca gta tgt tta tca tat cag tac    2240
Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr Gln Tyr
                680                 685                 690

tca gga ttg gaa gat act gta gag gac aag cag gaa gtg aat gtt ggg    2288
Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn Val Gly
        695                 700                 705
```

```
aaa cct ctc att gct aaa tta gac atg cat cga ggt ttg gga agg aag   2336
Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly Arg Lys
    710             715             720

act tgc ttt caa act tgt ctt atg tct aat ggt cct tac cag agt tct   2384
Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln Ser Ser
725             730             735             740

gca gcc acc tca gga gga gca ggg cat tat cac tca ttg caa gac cca   2432
Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln Asp Pro
            745             750             755

ttc cat ggt gtt tac cat tca cat cct ggt aat cca agt aat gtt aca   2480
Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn Val Thr
            760             765             770

cca gca gat agc tgt cat tgc agc cgg act cca gat gca ttt att tca   2528
Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe Ile Ser
            775             780             785

agt ttc gct cac cat gct tca tgt cat ttt agt aga agt aat gtg cca   2576
Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn Val Pro
    790             795             800

gta gag aca act gat gaa ata cca ttt agt ttc tct gac agg ctc aga   2624
Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg Leu Arg
805             810             815             820

att tct gaa aaa tgacctcctt gtttttgaaa gttagcataa ttttagatgc       2676
Ile Ser Glu Lys

ctgtgaaata gtactgcact tacataaagt gagacattgt gaaaaggcaa atttgtatat 2736

gtagagaaag aatagtagta actgtttcat agcaaacttc aggactttga gatgttgaaa 2796

ttacattatt taattacaga cttcctcttt ct                               2828


<210> 133
<211> 919
<212> PRT
<213> Homo sapiens

<400> 133
Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn Glu Thr
  1               5                   10                  15

Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro Val Ser
            20                  25                  30

Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu Asn Lys
            35                  40                  45

Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp
    50                  55                  60

Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys
```

243

Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser Val Leu
                85   90   95

Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile
                100   105   110

Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu
                115   120   125

Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu
    130   135   140

Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr
145   150   155   160

Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe
                165   170   175

Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr
                180   185   190

Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly
                195   200   205

Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg
    210   215   220

Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu
225   230   235   240

Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro Lys Thr
                245   250   255

Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser Phe Tyr
                260   265   270

Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu Leu Gly
                275   280   285

Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala Val Ala
    290   295   300

Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu Ala Leu
305   310   315   320

Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys Leu Pro
                325   330   335

Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp Lys Thr
                340   345   350

Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe Thr Ser
                355   360   365

Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln Phe Gly

244

Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala
385   390   395   400

Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala Val Ile
               405   410   415

Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu Ile Ala
               420   425   430

Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr Ile Arg
               435   440   445

Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys
               450   455   460

Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe Met Lys
465   470   475   480

Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln Ser Lys
               485   490   495

Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr Gln Gln
               500   505   510

Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala Leu Ala
               515   520   525

Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val Gly Ile
               530   535   540

Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr Leu Ile
545   550   555   560

Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln Glu Thr
               565   570   575

Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr Ser Gln
               580   585   590

Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln Leu Ser
               595   600   605

Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro Arg His
               610   615   620

Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val Val Ala
625   630   635   640

Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala Ala Asp
               645   650   655

Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys Glu Ala
               660   665   670

Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met Ser Ala

245

```
Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe Val Arg
    690                 695             700

Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser Leu Ala
705             710             715                 720

Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp
                725             730             735

Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu
            740             745             750

Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp Lys Asp
        755             760             765

Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile
    770             775             780

Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu Arg Asp
785             790             795                 800

Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys Phe Val
            805             810             815

Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr Lys Ser
        820             825             830

Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr Ala Val
        835             840             845

Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu
    850             855             860

Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe
865             870             875                 880

Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile Ile Lys
            885             890             895

Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser Ser Thr
        900             905             910

Ser Ser Ser Phe Leu Glu Val
        915
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<210> 134
<211> 3612
<212> DNA
<213> Homo sapiens

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<222> (427)..(3183)

<400> 134

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cctccccgcc cgccctctct ccctcccttc ctccctcccg ctcgcttctt ctcacgccgg 120

gagcaggctc ccgcctcgca ccgctgcccc gcgagcagct cctcttctcc cgaggcgcgc 180

ggggcgcccc cgcgagcccc gcggctgaga ccccgcagcc tggaggaggg ctgtccgggg 240

ctttggatgc tgctgctagg ggtggtggga gcagccgtgg acgcgtggc  cgggagcggg 300

ggtgacagcc tgggattccg ggggcttctc ttccttgtcc tcctcctctc ctctctattc 360

ccagtgtggc cgtggctgac actaaagact ttgtagccat caacccgagt gcagtttcga 420
```

```
tggaaa atg aag gtt gca cgt ttt caa aaa ata cct aat ggt gaa aat     468
       Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn
        1               5                   10
```

```
gag aca atg att cct gta ttg aca tca aaa aaa gca agt gaa tta cca     516
Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro
 15                  20                  25                  30
```

```
gtc agt gaa gtt gca agc att ctc caa gct gat ctt cag aat ggt cta     564
Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu
                35                  40                  45
```

```
aac aaa tgt gaa gtt agt cat agg cga gcc ttt cat ggc tgg aat gag     612
Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu
                50                  55                  60
```

```
ttt gat att agt gaa gat gag cca ctg tgg aag aag tat att tct cag     660
Phe Asp Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln
            65                  70                  75
```

```
ttt aaa aat ccc ctt att atg ctg ctt ctg gct tct gca gtc atc agt     708
Phe Lys Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser
         80                  85                  90
```

```
gtt tta atg cat cag ttt gat gat gcc gtc agt atc act gtg gca ata     756
Val Leu Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile
 95                  100                 105                 110
```

```
ctt atc gtt gtt aca gtt gcc ttt gtt cag gaa tat cgt tca gaa aaa     804
Leu Ile Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys
                115                 120                 125
```

```
tct ctt gaa gaa ttg agt aaa ctt gtg cca cca gaa tgc cat tgt gtg     852
Ser Leu Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val
                130                 135                 140
```

```
cgt gaa gga aaa ttg gag cat aca ctt gcc cga gac ttg gtt cca ggt     900
Arg Glu Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly
            145                 150                 155
```

```
gat aca gtt tgc ctt tct gtt ggg gat aga gtt cct gct gac tta cgc     948
Asp Thr Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg
```

247

ttg ttt gag gct gtg gat ctt tcc att gat gag tcc agc ttg aca ggt   996
Leu Phe Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly
175   180   185   190

gag aca acg cct tgt tct aag gtg aca gct cct cag cca gct gca act   1044
Glu Thr Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr
                195   200   205

aat gga gat ctt gca tcg aga agt aac att gcc ttt atg gga aca ctg   1092
Asn Gly Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu
                210   215   220

gtc aga tgt ggc aaa gca aag ggt gtt gtc att gga aca gga gaa aat   1140
Val Arg Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn
           225   230   235

tct gaa ttt ggg gag gtt ttt aaa atg atg caa gca gaa gag gca cca   1188
Ser Glu Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro
      240   245   250

aaa acc cct ctg cag aag agc atg gac ctc tta gga aaa caa ctt tcc   1236
Lys Thr Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser
255   260   265   270

ttt tac tcc ttt ggt ata ata gga atc atc atg ttg gtt ggc tgg tta   1284
Phe Tyr Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu
                275   280   285

ctg gga aaa gat atc ctg gaa atg ttt act att agt gta agt ttg gct   1332
Leu Gly Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala
                290   295   300

gta gca gca att cct gaa ggt ctc ccc att gtg gtc aca gtg acg cta   1380
Val Ala Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu
                305   310   315

gct ctt ggt gtt atg aga atg gtg aag aaa agg gcc att gtg aaa aag   1428
Ala Leu Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys
      320   325   330

ctg cct att gtt gaa act ctg ggc tgc tgt aat gtg att tgt tca gat   1476
Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp
335   340   345   350

aaa act gga aca ctg acg aag aat gaa atg act gtt act cac ata ttt   1524
Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe
                355   360   365

act tca gat ggt ctg cat gct gag gtt act gga gtt ggc tat aat caa   1572
Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln
                370   375   380

ttt ggg gaa gtg att gtt gat ggt gat gtt gtt cat gga ttc tat aac   1620
Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn
      385   390   395

248

```
cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct      1668
Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala
    400             405                 410

gta att aga aac aat act cta atg ggg aag cca aca gaa ggg gcc tta      1716
Val Ile Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu
415                 420                 425                 430

att gct ctt gca atg aag atg ggt ctt gat gga ctt caa caa gac tac      1764
Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr
                435                 440                 445

atc aga aaa gct gaa tac cct ttt agc tct gag caa aag tgg atg gct      1812
Ile Arg Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala
                450                 455                 460

gtt aag tgt gta cac cga aca cag cag gac aga cca gag att tgt ttt      1860
Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe
            465                 470                 475

atg aaa ggt gct tac gaa caa gta att aag tac tgt act aca tac cag      1908
Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln
    480                 485                 490

agc aaa ggg cag acc ttg aca ctt act cag cag cag aga gat gtg tac      1956
Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr
495                 500                 505                 510

caa caa gag aag gca cgc atg ggc tca gcg gga ctc aga gtt ctt gct      2004
Gln Gln Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala
                515                 520                 525

ttg gct tct ggt cct gaa ctg gga cag ctg aca ttt ctt ggc ttg gtg      2052
Leu Ala Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val
                530                 535                 540

gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca      2100
Gly Ile Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr
            545                 550                 555

ctc att gcc tca gga gta tca ata aaa atg att act gga gat tca cag      2148
Leu Ile Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln
    560                 565                 570

gag act gca gtt gca atc gcc agt cgt ctg gga ttg tat tcc aaa act      2196
Glu Thr Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr
575                 580                 585                 590

tcc cag tca gtc tca gga gaa gaa ata gat gca atg gat gtt cag cag      2244
Ser Gln Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln
                595                 600                 605

ctt tca caa ata gta cca aag gtt gca gta ttt tac aga gct agc cca      2292
Leu Ser Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro
                610                 615                 620    .
```

249

```
agg cac aag atg aaa att att aag tcg cta cag aag aac ggt tca gtt    2340
Arg His Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val
        625                 630                 635

gta gcc atg aca gga gat gga gta aat gat gca gtt gct ctg aag gct    2388
Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala
        640                 645                 650

gca gac att gga gtt gcg atg ggc cag act ggt aca gat gtt tgc aaa    2436
Ala Asp Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys
655                 660                 665                 670

gag gca gca gac atg atc cta gtg gat gat gat ttt caa acc ata atg    2484
Glu Ala Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met
            675                 680                 685

tct gca atc gaa gag ggt aaa ggg att tat aat aac att aaa aat ttc    2532
Ser Ala Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe
            690                 695                 700

gtt aga ttc cag ctg agc acg agt ata gca gca tta act tta atc tca    2580
Val Arg Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser
        705                 710                 715

ttg gct aca tta atg aac ttt cct aat cct ctc aat gcc atg cag att    2628
Leu Ala Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile
        720                 725                 730

ttg tgg atc aat att att atg gat gga ccc cca gct cag agc ctt gga    2676
Leu Trp Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly
735                 740                 745                 750

gta gaa cca gtg gat aaa gat gtc att cgt aaa cct cct cgc aac tgg    2724
Val Glu Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp
                755                 760                 765

aaa gac agc att ttg act aaa aac ttg ata ctt aaa ata ctt gtt tca    2772
Lys Asp Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser
            770                 775                 780

tca ata atc att gtt tgt ggg act ttg ttt gtc ttc tgg cgt gag cta    2820
Ser Ile Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu
            785                 790                 795

cga gac aat gtg att aca cct cga gac aca aca atg acc ttc aca tgc    2868
Arg Asp Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys
        800                 805                 810

ttt gtg ttt ttt gac atg ttc aat gca cta agt tcc aga tcc cag acc    2916
Phe Val Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr
815                 820                 825                 830

aag tct gtg ttt gag att gga ctc tgc agt aat aga atg ttt tgc tat    2964
Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr
                835                 840                 845

gca gtt ctt gga tcc atc atg gga caa tta cta gtt att tac ttt cct    3012
```

250

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    Ala Val Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro
                    850                 855                 860

ccg ctt cag aag gtt ttt cag act gag agc cta agc ata ctg gat ctg   3060
Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu
            865                 870                 875

ttg ttt ctt ttg ggt ctc acc tca tca gtg tgc ata gtg gca gaa att   3108
Leu Phe Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile
        880                 885                 890

ata aag aag gtt gaa agg agc agg gaa aag atc cag aag cat gtt agt   3156
Ile Lys Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser
895                 900                 905                 910

tcg aca tca tca tct ttt ctt gaa gta tgatgcatat tgcattattt        3203
Ser Thr Ser Ser Ser Phe Leu Glu Val
                915

tatttgcaaa ctaggaattg cagtctgagg atcatttaga agggcaagtt caagaggata 3263

tgaagatttg agaacttttt aactattcat tgactaaaaa tgaacattaa tgttaaagac 3323

ttaagacttt aacctgctgg cagtcccaaa tgaaattatg caactttgat atcatattcc 3383

ttgatttaaa ttggcttttg tgattgagtg aaactttata aagcatatgg tcagttattt 3443

aattaaaaag gcaaaacctg aaccaccttc tgcacttaaa gaagtctaac agtacaaata 3503

cactatctat cttagataga tatatttttt tttatttta aatattgtac tatttatggt 3563

ggtggggctt tcttactaat acacaaataa atttaatcat ttcaaaggc            3612


<210> 135
<211> 382
<212> PRT
<213> Homo sapiens

<400> 135
Met Gly Ala Phe Leu Asp Lys Pro Lys Met Glu Lys His Asn Ala Gln
 1               5                  10                  15

Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu Ser Ser Met Gln Gly Trp
            20                  25                  30

Arg Val Glu Met Glu Asp Ala His Thr Ala Val Ile Gly Leu Pro Ser
            35                  40                  45

Gly Leu Glu Ser Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly
        50                  55                  60

Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr
65                  70                  75                  80

Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly Ala Pro Ser Val Glu Asn
                85                  90                  95
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251

Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met
            100   105   110

Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr
            115   120   125

Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys
            130   135   140

Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe
145   150   155   160

Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln
                165   170   175

Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala
            180   185   190

Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys
            195   200   205

Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro Glu Val His Asp Ile
            210   215   220

Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly
225   230   235   240

Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser
                245   250   255

Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val
                260   265   270

Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu
            275   280   285

Ile Cys Phe Pro Asn Ala Pro Lys Val Ser Pro Glu Ala Val Lys Lys
            290   295   300

Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys Arg Val Glu Glu Ile Ile
305   310   315   320

Lys Lys Gln Gly Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr
                325   330   335

Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala
            340   345   350

Ser Lys Arg Asn Val Ile Glu Ala Val Tyr Asn Arg Leu Asn Pro Tyr
            355   360   365

Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr Asp Asp Met Trp
            370   375   380

<210> 136

252

<211> 2467
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (444)..(1589)

<400> 136
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cgggtcctca ggcggctgtt gctccggaac gggtggttgg ggagggggg gtggggggac 120

tctagacagc tgaggcgcga aagcgatgag tcctcggctc ttcctcctcc ttctccggga 180

cccgctctct gcctccctct ccaacgcccg gatgatctga gccgcgaggg cgccgacagc 240

cggggcccg gacgcagccc ggctcctccc ctcctccgcc ccttccccag cctgacctgg 300

cccgccgctg cagcggtgac ccctcccccg gctgccgccg tcgccgccgc ggtgaccccc 360

tccccggctg ccgccgccgc cgcctcggcc gaccagggac ctgcccgcct gcggctgctc 420

cggacctaga ggatcaagac ata atg gga gca ttt tta gac aag cca aag atg 473
                          Met Gly Ala Phe Leu Asp Lys Pro Lys Met
                           1   5   10

gaa aag cat aat gcc cag ggg cag ggt aat ggg ttg cga tat ggg cta   521
Glu Lys His Asn Ala Gln Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu
              15   20   25

agc agc atg caa ggc tgg cgt gtt gaa atg gag gat gca cat acg gct   569
Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala
              30   35   40

gtg atc ggt ttg cca agt gga ctt gaa tcg tgg tca ttc ttt gct gtg   617
Val Ile Gly Leu Pro Ser Gly Leu Glu Ser Trp Ser Phe Phe Ala Val
              45   50   55

tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat   665
Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His
        60   65   70

ttg tta gat cac atc acc aat aac cag gat ttt aaa ggg tct gca gga   713
Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly
 75   80   85   90

gca cct tct gtg gaa aat gta aag aat gga atc aga aca ggt ttt ctg   761
Ala Pro Ser Val Glu Asn Val Lys Asn Gly Ile Arg Thr Gly Phe Leu
                  95   100   105

gag att gat gaa cac atg aga gtt atg tca gag aag aaa cat ggt gca   809
Glu Ile Asp Glu His Met Arg Val Met Ser Glu Lys Lys His Gly Ala
                  110   115   120

gat aga agt ggg tca aca gct gta ggt gtc tta att tct ccc caa cat   857
Asp Arg Ser Gly Ser Thr Ala Val Gly Val Leu Ile Ser Pro Gln His

```
act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac    905
Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn
    140             145             150

agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg    953
Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu
155             160             165             170

gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt   1001
Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg
                175             180             185

gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac   1049
Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr
            190             195             200

aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag   1097
Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu
        205             210             215

cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att   1145
Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile
    220             225             230

atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc   1193
Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu
235             240             245             250

tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa   1241
Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys
            255             260             265

gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac   1289
Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp
            270             275             280

aac atg agt gtg att ttg atc tgt ttt cca aat gca ccc aaa gta tcg   1337
Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser
        285             290             295

cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc   1385
Pro Glu Ala Val Lys Lys Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys
    300             305             310

aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta   1433
Arg Val Glu Glu Ile Ile Lys Lys Gln Gly Glu Gly Val Pro Asp Leu
315             320             325             330

gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca   1481
Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro
            335             340             345

cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac   1529
Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr
            350             355             360
```

254

```
aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca   1577
Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr
        365                 370                 375

gat gat atg tgg taaaactgct catctagcca tggagtttac cttcacctcc       1629
Asp Asp Met Trp
        380

aaaggagagt acagctcaac tttgttgaaa cttttaacat ccatcctcaa ctttaaggaa 1689

ggggatatga catgggtgag aatgattaca tcagagaact tcagcagtac aacagctagc 1749

ccagaactga tttttttttt tttttgtaa atttgagact tatgtaagcg tgatttcaaa 1809

ccataattcg tgttgtaaat cagactccag caatttttgt tgtatgattt tgttttttg  1869

taaagtgtaa ttgtccttgt acaaaatgct catatttaat tatgaactgc tttaaatcac 1929

tatcaaagtt acaagaaatg tttggcttat tgtgtgatgc aacagatata tagccctttc 1989

aagtcatgtt gtgtttggac ttggggttgg aacagggaga gcagcagcca tgtcagctac 2049

acgctcaaat gtgcagatga ttatggaaaa taacctcaaa atcttacaaa gctgaacatc 2109

caaggagtta ttgaaaacta tcttaaatgt tcttggtagg ggagttggca ttgttgataa 2169

agccagtccc ttcatttaac tgtctttcag gatgttcctt cgttgtttcc atgagtattg 2229

caggtaataa tacagtgtat tcataagaat ctcaatcttg gggctaaatg ccttgtttct 2289

ttgcacctct tttcaagtcc ttacatttaa ttactaattg ataagcagca gcttcctaca 2349

tatagtagga aactgccaca tttttgctat catgattggc tgggcctgct gctgttccta 2409

gtaagatatt ctgaattcca ttttatcaat aaagcttgat ttaacaaaca agaaactt    2467


<210> 137
<211> 358
<212> PRT
<213> Homo sapiens

<400> 137
Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val
  1               5                  10                  15

Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp
            20                  25                  30

Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu
            35                  40                  45

Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val
    50                  55                  60

Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg
```

255

Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn
            85   90   95

Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser
            100   105   110

Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser
            115   120   125

Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met
    130   135   140

Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala
145   150   155   160

Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser
            165   170   175

Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr
            180   185   190

Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln
            195   200   205

Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln
    210   215   220

Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro
225   230   235   240

Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln
            245   250   255

Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln
            260   265   ,   270

Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr
            275   280   285

Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln
    290   295   300

Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly
305   310   315   320

Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro
            325   330   335

Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln
            340   345   350

Pro Gly Pro Gly Tyr Arg
            355

256

<210>_138
<211> 1519
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (11)..(1084)

<400> 138
attagtgcta atg atg caa cga gtt ttc aga gga aaa ctt ctg agt aat   49
          Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn
           1   5   10

gat gaa gta aca ata aag tat aaa gat gaa gat gga gat ctt ata aca   97
Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr
   15   20   25

att ttt gat agt tct gac ctt tcc ttt gca att cag tgc agt agg ata   145
Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile
 30   35   40   45

ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca   193
Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser
                50   55   60

agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa   241
Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys
                65   70   75

gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct   289
Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro
           80   85   90

tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag   337
Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys
        95   100   105

tct gct tct gat tct tct gga aaa cag tct act cag gtt atg gca gca   385
Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala
110   115   120   125

agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa   433
Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys
                130   135   140

aat gtt atg tca gcg ttt ggc tta aca gat gat cag gtt tca ggg cca   481
Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro
                145   150   155

ccc agt gct cct gca gaa gat cgt tca gga aca ccc gac agc att gct   529
Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala
           160   165   170

tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca   577
Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro
   175   180   185

257

```
cca tat aca gga gct cag act caa gca ggt cag atg tac caa cag tac    625
Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr
190             195             200             205

cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag    673
Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln
            210             215             220

cag cct caa cag tat ggt att cag tat tca gca agc tat agt cag cag    721
Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln
            225             230             235

act gga ccc caa caa cct cag cag ttc cag gga tat ggc cag caa cca    769
Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro
        240             245             250

act tcc cag gca cca gct cct gcc ttt tct ggt cag cct caa caa ctg    817
Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu
    255             260             265

cct gct cag ccg cca cag cag tac cag gcg agc aat tat cct gca caa    865
Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln
270             275             280             285

act tac act gcc caa act tct cag cct act aat tat act gtg gct cct    913
Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro
            290             295             300

gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca    961
Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro
            305             310             315

aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca    1009
Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro
        320             325             330

agt ggg cct aat cct tat gcg cgt aac cgt cct ccc ttt ggt cag ggc    1057
Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly
    335             340             345

tat acc caa cct gga cct ggt tat cga taaggaggct cctctacacc          1104
Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
350             355

aattaatgta gctgctagct attggcctcc caaaagactc cagtactatt ttaatttgta  1164

ttgaagaagt tcagaaattt aaaagcagag catttttat gatatcattg ttggtgttaa   1224

ttgaaagtat aatttgctgg aacacaaaga ccaaaatgaa agttttttcc tccctgctta   1284

aaaatgtagc agcttcttag ttactttgga acactactct tacatgtata aagtgattga   1344

cttgactttc tagcttccct tgtccggagg atattaaaat gctagggtga ggtttagcca   1404

tcttacttgg ctttttacta ttaacatgat gtactaaagt agagcccttt gagaatacaa   1464
```

gatattatgt ataaaatgta acactgatga taggttaata aagatgattg aatcc   1519

<210> 139
<211> 396
<212> PRT
<213> Homo sapiens

<400> 139
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Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu Ile Val Lys Ala Gln
 1               5                  10                  15

Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His Asn Glu Asp Ile Thr
            20                  25                  30

Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val Phe Arg Gly Lys Leu
        35                  40                  45

Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp
    50                  55                  60

Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys
65                  70                  75                  80

Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro
                85                  90                  95

Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu
            100                 105                 110

Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu
            115                 120                 125

Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg
        130                 135                 140

Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val
145                 150                 155                 160

Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu
                165                 170                 175

Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val
            180                 185                 190

Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp
            195                 200                 205

Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro
    210                 215                 220

Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr
225                 230                 235                 240

Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala
                245                 250                 255
```

259

```
Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr
        260             265             270

Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly
        275             280             285

Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro
    290             295             300

Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr
305             310             315             320

Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr
            325             330             335

Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala
        340             345             350

Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr
        355             360             365

Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe
    370             375             380

Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
385             390             395


<210> 140
<211> 1641
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (19)..(1206)

<400> 140
aacatcctgg agtccacc atg aac gga cag ttg gat cta agt ggg aag cta    51
                    Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu
                     1           5                  10

atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat    99
Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His
            15                  20                  25

aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt   147
Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val
            30                  35                  40

ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag tat aaa   195
Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys
        45                  50                  55

gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc   243
Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser
60                  65                  70                  75
```

```
ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat    291
Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn
                80                  85                  90

ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga    339
Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg
            95                  100                 105

gaa ctg ata gaa ctt cga aat aaa gtg aat cgt tta ttg gat agc ttg    387
Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu
            110                 115                 120

gaa cca cct gga gaa cca gga cct tcc acc aat att cct gaa aat gat    435
Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp
        125                 130                 135

act gtg gat ggt agg gaa gaa aag tct gct tct gat tct tct gga aaa    483
Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys
140                 145                 150                 155

cag tct act cag gtt atg gca gca agt atg tct gct ttt gat cct tta    531
Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu
                160                 165                 170

aaa aac caa gat gaa atc aat aaa aat gtt atg tca gcg ttt ggc tta    579
Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu
            175                 180                 185

aca gat gat cag gtt tca ggg cca ccc agt gct cct gca gaa gat cgt    627
Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg
        190                 195                 200

tca gga aca ccc gac agc att gct tcc tcc tcc tca gca gct cac cca    675
Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro
        205                 210                 215

cca ggc gtt cag cca cag cag cca cca tat aca gga gct cag act caa    723
Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln
220                 225                 230                 235

gca ggt cag atg tac caa cag tac cag caa cag gcc ggc tat ggt gca    771
Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala
                240                 245                 250

cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag    819
Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln
            255                 260                 265

tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag    867
Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln
            270                 275                 280

ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc    915
Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala
        285                 290                 295
```

261

```
ttt tct ggt cag cct caa caa ctg cct gct cag ccg cca cag cag tac  963
Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr
300                 305             310                 315

cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag  1011
Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln
                320             325                 330

cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca  1059
Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro
                335             340                 345

agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct  1107
Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro
        350             355             360

gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt  1155
Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg
    365             370             375

aac cgt cct ccc ttt ggt cag ggc tat acc caa cct gga cct ggt tat  1203
Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr
380             385             390                 395

cga taaggaggct cctctacacc aattaatgta gctgctagct attggcctcc        1256
Arg

caaaagactc cagtactatt ttaatttgta ttgaagaagt tcagaaattt aaaagcagag 1316

catttttat gatatcattg ttggtgttaa ttgaaagtat aatttgctgg aacacaaaga 1376

ccaaaatgaa agttttttcc tccctgctta aaaatgtagc agcttcttag ttactttgga 1436

acactactct tacatgtata aagtgattga cttgactttc tagcttccct tgtccggagg 1496

atattaaaat gctagggtga ggtttagcca tcttacttgg ctttttacta ttaacatgat 1556

gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta acactgatga 1616

taggttaata aagatgattg aatcc                                       1641
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<210> 141
<211> 323
<212> PRT
<213> Homo sapiens

<400> 141
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Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro
 1               5                   10                  15

Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr
            20                  25                  30

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn
            35                  40                  45
```

262

```
Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro
    50              55                  60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly
65              70                  75                  80

Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly
                85                  90                  95

Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val
            100                 105                 110

Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
            115                 120                 125

His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
        130                 135                 140

Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
145                 150                 155                 160

Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe
            165                 170                 175

Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
            180                 185                 190

Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
        195                 200                 205

Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile
    210                 215                 220

Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe
225                 230                 235                 240

Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
            245                 250                 255

Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
            260                 265                 270

Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala
        275                 280                 285

Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu
    290                 295                 300

Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His
305                 310                 315                 320

Val Gln Thr
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<210> 142
<211> 1616

263

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (72)..(1040)

<400> 142
aagtcgttcc ctctacaaag gacttcctag tgggtgtgaa aggcagcggt ggccacagag 60

gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca   110
            Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro
            1   5   10

gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag gac gga ctt   158
Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu
    15   20   25

cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga acc agg ttt   206
Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe
30   35   40   45

gct gtg aac ttt cag act ggc ttc agt gga aat gac att gcc ttc cac   254
Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His
                50   55   60

ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc aac acg agg   302
Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg
                65   70   75

cag aac gga agc tgg ggg ccc gag gag agg aag aca cac atg cct ttc   350
Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe
            80   85   90

cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag agc tca gat   398
Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp
        95   100   105

ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac ttc cac cgc   446
Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg
110   115   120   125

gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag   494
Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln
            130   135   140

ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg   542
Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro
                145   150   155

gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga   590
Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly
            160   165   170

cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc   638
Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro
        175   180   185

264

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gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca    686
Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro
190             195             200             205

tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg    734
Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg
            210             215             220

ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac    782
Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn
            225             230             235

ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac    830
Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn
        240             245             250

tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc    878
Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val
    255             260             265

cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc    926
Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu
270             275             280             285

aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg    974
Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu
            290             295             300

agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag    1022
Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln
            305             310             315

ctg acc cat gtg cag aca taggcggctt cctggccctg gggccggggg          1070
Leu Thr His Val Gln Thr
        320

ctggggtgtg gggcagtctg ggtcctctca tcatccccac ttcccaggcc cagcctttcc  1130

aaccctgcct gggatctggg ctttaatgca gaggccatgt ccttgtctgg tcctgcttct  1190

ggctacagcc accctggaac ggagaaggca gctgacgggg attgccttcc tcagccgcag  1250

cagcacctgg ggctccagct gctggaatcc taccatccca ggaggcaggc acagccaggg  1310

agaggggagg agtgggcagt gaagatgaag ccccatgctc agtcccctcc catcccccac  1370

gcagctccac cccagtccca agccaccagc tgtctgctcc tggtgggagg tggcctcctc  1430

agcccctcct ctctgacctt taacctcact ctcaccttgc accgtgcacc aacccttcac  1490

ccctcctgga aagcaggcct gatggcttcc cactggcctc caccacctga ccagagtgtt  1550

ctcttcagag gactggctcc tttcccagtg tccttaaaat aaagaaatga aaatgcttgt  1610

tggcac                                                            1616
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<210> 143
<211> 136
<212> PRT
<213> Homo sapiens

<400> 143
Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile
1   5   10   15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
                20   25   30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
            35   40   45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
        50   55   60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65   70   75   80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
                85   90   95

Pro Leu Pro His Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His
            100   105   110

Gly His Leu Ser Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe
        115   120   125

Leu Gln Pro Leu Met His Cys Val
    130   135

<210> 144
<211> 1252
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (225)..(632)

<400> 144
acaatcacag ctccgggcat tggggggaacc cgagccggct gcgccggggg aatccgtgcg   60

ggcgccttcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236
                                                Met Ala Gly Ala
                                                1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

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ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct   332
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
                25              30              35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat   380
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
            40              45              50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc   428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
        55              60              65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa   476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
    70              75              80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac   524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
 85              90              95             100

atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca   572
Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser
                105             110             115

gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta   620
Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu
                120             125             130

atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca   672
Met His Cys Val
        135

ttgttaatta gtgacatagt aacatctgta gcagctggtt agtaaacctc atgtggggt 732

ggggtggggg tgtattcctt gggggatggt ttgggccgaa tgggagtgg aatatttgac 792

atttttcctg ttttaaattc taggatagat tttaacatcc tttgcggtcc cagtccaagg 852

taggctggtg tcatagtctt ctcactccta atccatgacc actgtttttt tcctatttat 912

atcaccaggt agcctactga gttaatattt aagttgtcaa tagataagtg tccctgtttt 972

gtggcataat ataactgaat ttcatgagaa gatttattcc accaggggta tttcagcttt 1032

gaaaccaaat ctgtgtatct aatactaacc aatctgttgg atgtgggttt taaaaaatgt 1092

ttgctaaact acccaagtaa gatttactgt attaaatggc cttcgggtct gaaaagcttt 1152

tttaacctct tgcttaaaat gcgttttatt ttgataagat acttcaaata gcctccaaaa 1212

gtgtagatcc aatcacttaa ataaacctgt atgtatatgc 1252
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<210> 145
<211> 468
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267

<212> PRT
<213> Homo sapiens

<400> 145
Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp
1   5   10   15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Phe
            20   25   30

Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln
        35   40   45

Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg
    50   55   60

Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro
65   70   75   80

Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu
                85   90   95

Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser
            100   105   110

Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu
        115   120   125

Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu
        130   135   140

Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met
145   150   155   160

Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp
                165   170   175

Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val
                180   185   190

Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu
        195   200   205

Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp
    210   215   220

Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile
225   230   235   240

Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala
                245   250   255

Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu
            260   265   270

Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe
        275   280   285

268

Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe
    290   295   300

Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys
305   310   315   320

Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser
            325   330   335

Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile
            340   345   350

Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met
            355   360   365

Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys
    370   375   380

Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile
385   390   395   400

Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala
            405   410   415

Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu
            420   425   430

Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr
            435   440   445

Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala
    450   455   460

Ala Ser Gly Ile
465

<210> 146
<211> 1943
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (379)..(1782)

<400> 146
acaatcacag ctccgggcat tgggggaacc cgagccggct gcgccggggg aatccgtgcg 60

ggcgccttcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa ggggggggcgc aaaaatggct ggggcaatta 240

tagaaaacat gagcaccaag aagctgtgca ttgttggtgg gattctgctc gtgttccaaa 300

269

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tcatcgcctt tctggtggga ggcttgattg ctccagggcc cacaacggca gtgtcctaca 360

tgtcggtgaa atgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt     411
                     Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly
                      1           5                  10

tcg tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag     459
Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys
            15              20              25

agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gac att gcc ttc     507
Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe
        30              35              40

aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt     555
Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val
    45              50              55

tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc     603
Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala
60              65              70                  75

cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag     651
His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys
                80              85              90

act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc     699
Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe
            95              100             105

atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg     747
Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg
        110             115             120

ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag·ata     795
Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile
    125             130             135

aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag     843
Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys
140             145             150             155

gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att     891
Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile
            160             165             170

atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg     939
Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val
            175             180             185

ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc     987
Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile
        190             195             200

aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg     1035
Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met
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270

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ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg   1083
Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu
220             225             230             235

tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gat cag cac gag   1131
Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu
                240             245             250

cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt   1179
Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val
                255             260             265

ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa   1227
Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln
                270             275             280

ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag   1275
Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu
                285             290             295

ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac   1323
Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr
300             305             310             315

ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt   1371
Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser
                320             325             330

ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac   1419
Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His
                335             340             345

tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg   1467
Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu
                350             355             360

gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg   1515
Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr
                365             370             375

gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc   1563
Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala
380             385             390             395

ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg   1611
Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu
                400             405             410

atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc   1659
Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser
                415             420             425

aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt   1707
Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe
                430             435             440
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271

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gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc    1755
Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe
    445             450             455

atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca         1802
Ile Asn Asp Asn Ala Ala Ser Gly Ile
460             465

tgtttatcag ctttgcattt gcagttgtca cagtcacatt gattgtactt gtatacgcac 1862

acaaatacac tcatttagcc tttatctcaa aatgttaaat ataaggaaaa aagcgtcaac 1922

aataaatatt ctttgagtat t                                            1943


<210> 147
<211> 460
<212> PRT
<213> Homo sapiens

<400> 147
Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp
  1             5                 10                  15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Gly
              20                25                  30

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro
          35                40                45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr
      50                55                60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr
  65                70                75                80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val
              85                90                95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu
              100               105               110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile
          115               120               125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly
      130               135               140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile
145               150               155               160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg
              165               170               175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met
          180               185               190
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272

```
Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp
    195                 200                 205

Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala
    210                 215                 220

Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp
225                 230                 235                 240

Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro
            245                 250                 255

Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg
            260                 265                 270

Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile
            275                 280                 285

Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu
            290                 295                 300

Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg
305                 310                 315                 320

Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg
            325                 330                 335

Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu
            340                 345                 350

Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser
            355                 360                 365

Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile Thr Val Gln Val
            370                 375                 380

Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val
385                 390                 395                 400

Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu
            405                 410                 415

Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys
            420                 425                 430

Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys
            435                 440                 445

Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
    450                 455                 460


<210> 148
<211> 1919
<212> DNA
<213> Homo sapiens
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273

<220>
<221> CDS
<222> (376)..(1755)

<400> 148
atcacagctc cgggcattgg gggaacccga gccggctgcg ccgggggaat ccgtgcgggc 60

gccttccgtc ccggtcccat cctcgccgcg ctccagcacc tctgaagttt tgcagcgccc 120

agaaaggagg cgaggaagga gggagtgtat gagaggaggg agcaaaaagc tcaccctaaa 180

acatttattt caaggagaaa agaaaaaggg ggggcgcaaa aatggctggg gcaattatag 240

aaaacatgag caccaagaag ctgtgcattg ttggtgggat tctgctcgtg ttccaaatca 300

tcgcctttct ggtgggaggc ttgattgctc agggcccac aacggcagtg tcctacatgt 360

cggtgaaatg tgtgg atg ccc gta aga acc atc aca aga caa aat ggt tcg 411
              Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser
                1   5   10

tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg 459
Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg
        15   20   25

caa ttc caa ggg aaa ttg aag cca atg aca tcg tgt ttt ctg ttc aca 507
Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr
   30   35   40

ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt 555
Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe
45   50   55   60

gct gag tgg act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa 603
Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys
             65   70   75

tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat 651
Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr
           80   85   90

gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag 699
Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys
         95   100   105

ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc 747
Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile
   110   115   120

aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac 795
Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His
125   130   135   140

caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt 843
Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu
             145   150   155

274

```
acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc    891
Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr
            160                 165                 170

atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt    939
Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu
            175                 180                 185

ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc    987
Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile
            190                 195                 200

ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag ggc   1035
Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly
205                 210                 215                 220

atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag   1083
Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu
                225                 230                 235

cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag   1131
His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys
                240                 245                 250

caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac   1179
Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp
            255                 260                 265

atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg   1227
Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp
270                 275                 280

act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct   1275
Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala
285                 290                 295                 300

gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt   1323
Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe
                305                 310                 315

cag gtg ttt cgg aac atc agt ggg aag cag tcc agc ctg cca gct atg   1371
Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met
                320                 325                 330

agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag   1419
Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys
            335                 340                 345

ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc   1467
Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe
            350                 355                 360

ttc atc gtt agt cag gta acg gaa ggc cat tgg aaa tgg ggc ggc atc   1515
Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile
365                 370                 375                 380
```

275

```
aca gtc caa gtg aac agt gcc ttt ttc aca ggc atc tat ggg atg tgg   1563
Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp
                385                 390                 395

aat ctg tat gtc ttt gct ctg atg ttc ttg tat gca cca tcc cat aaa   1611
Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys
                400                 405                 410

aac tat gga gaa gac cag tcc aat gga atg caa ctc cca tgt aaa tcg   1659
Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser
                415                 420                 425

agg gaa gat tgt gct ttg ttt gtt tcg gaa ctt tat caa gaa ttg ttc   1707
Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe
        430                 435                 440

agc gct tcg aaa tat tcc ttc atc aat gac aac gca gct tct ggt att   1755
Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
445                 450                 455                 460

tgagtcaaca aggcaacaca tgtttatcag ctttgcattt gcagttgtca cagtcacatt 1815

gattgtactt gtatacgcac acaaatacac tcatttagcc tttatctcaa aatgttaaat 1875

ataaggaaaa aagcgtcaac aataaatatt ctttgagtat tgtc           1919


<210> 149
<211> 183
<212> PRT
<213> Homo sapiens

<400> 149
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 1               5               10              15

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
            20              25              30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
            35              40              45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
    50              55              60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
65              70              75              80

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
            85              90              95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
            100             105             110

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
        115             120             125
```

```
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
    130             135             140
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
145             150             155             160
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
                165             170             175
Asp Arg His Lys Met Leu Ser
                180
```

<210> 150
<211> 1562
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (120)..(668)

<400> 150
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tacggctgcg agaagacgac agaagggggat taagagggag ggcggggaca actgggtctt 60

ttgcggctgc agcgggcttg taggtgtccg gctttgctgg cccagcaagc ctgataagc 119

atg aag ctc tta tct ttg gtg gct gtg gtc ggg tgt ttg ctg gtg ccc 167
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 1               5                   10                  15

cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 215
Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
            20                  25                  30

tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat gta 263
Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
        35                  40                  45

tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 311
Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
    50                  55                  60

cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac 359
Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
65                  70                  75                  80

gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg 407
Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
                85                  90                  95

tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg 455
Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
                100                 105                 110

gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat 503
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
```

```
gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc    551
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
    130                 135                 140

ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc    599
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
145                 150                 155                 160

cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc    647
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
                165                 170                 175

gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc      698
Asp Arg His Lys Met Leu Ser
                180
```

```
ccaacaccat ggctgccagc ttccaggctg acaaagcag ggggctactt ctcccttccc 758

tcggttccag tcttcccttt aaaagcctgt ggcatttttc ctccttctcc ctaactttag 818

aaatgttgta cttggctatt ttgattaggg aagagggatg tggtctctga tctccgttgt 878

cttcttgggt ctttggggtt gaagggaggg ggaaggcagg ccagaaggga atggagacat 938

tcgaggcggc ctcaggagtg gatgcgatct gtctctcctg ctccactct tgccgccttc 998

cagctctgag tcttgggaat gttgttaccc ttggaagata aagctgggtc ttcaggaact 1058

cagtgtctgg gaggaaagca tggcccagca ttcagcatgt gttcctttct gcagtggttc 1118

tttatcacca cctccctccc agccccagcg cctcagcccc agccccagct ccagccctga 1178

ggacagctct gatgggagag ctgggcccc tgagcccact gggtcttcag ggtgcactgg 1238

aagctggtgt cgctgtccc ctgtgcactt ctcgcactgg ggcatggagt gcccatgcat 1298

actctgctgc cggtcccctc acctgcactt gaggggtctg ggcagtccct cctctcccca 1358

gtgtccacag tcactgagcc agacggtcgg ttggaacatg agactcgagg ctgagcgtgg 1418

atctgaacac cacagcccct gtacttgggt tgcctcttgt ccctgaactt cgttgtacca 1478

gtgcatggag agaaaatttt gtcctcttgt cttagagttg tgtgtaaatc aaggaagcca 1538

tcattaaatt gttttatttc tctc                                        1562
```

```
<210> 151
<211> 2815
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (192)..(2387)
```

278

<400> 151

tctctcctcc tcctccagca gccaccaggg accgggagat ctaccagctc aagacccta 60

cagccaggtc tgtgctgccg ccctccagca tctttgcagc aggggacgag gctgtgtggg 120

aggctgtcgg ttcggaacat gtctccaccc accccaccct ctgtggctcc aggcttcatt 180

ctccccatc c atg gat aac cca ggg cct tcg ctc cgt ggt gcc ttt ggc 230
            Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly
             1   5   10

att cta ggt gcc ttg gaa agg gac agg ctg acc cac ctg aaa cac aag 278
Ile Leu Gly Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys
     15   20   25

ctg ggg agt ctg tgt tca ggc agc cag gag tca aag ctt ctc cat gcc 326
Leu Gly Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala
 30   35   40   45

atg gta ctc ctg gct ctg ggc cag gac acg gag gcc agg gtc tct ctg 374
Met Val Leu Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu
                 50   55   60

gag tcc ttg aag atg aac aca gta gcc cag ctg gta gcc cac cag tgg 422
Glu Ser Leu Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp
             65   70   75

gca gac atg gag acc aca gag ggc cct gag gag cct cca gac ttg tcc 470
Ala Asp Met Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser
             80   85   90

tgg acg gtg gct cgc ctg tac cac ctg ctg gct gag gag aac ctg tgt 518
Trp Thr Val Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys
     95   100   105

ccg gcc tct aca agg gac atg gct tac cag gtg gcc ctt cgt gac ttt 566
Pro Ala Ser Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe
110   115   120   125

gcc tcc cag ggt gac cac cag ctg ggc caa ctc cag aat gag gcc tgg 614
Ala Ser Gln Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp
                 130   135   140

gat cgg tgc agt tca gat atc aag ggg gac ccc agt ggt ttc cag cca 662
Asp Arg Cys Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro
             145   150   155

ctc cat tct cat cag ggt tcc ctg cag cca cct tca gca tcc cct gca 710
Leu His Ser His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala
             160   165   170

gtg acc aga agc cag cct cgt ccc att gac aca cca gac tgg agt tgg 758
Val Thr Arg Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp
     175   180   185

gga cat acg tta cac tcc acc aac agc act gcc tca ctg gcc agc cac 806

279

```
---Gly-His Thr Leu -His-Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His
   190              195              200              205

cta gag atc agc cag tca ccc act ctt gcc ttt ctc tct tca cac cat      854
Leu Glu Ile Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His
            210              215              220

gga acc cat ggg ccc agc aag cta tgt aac aca ccg ctg gac act cag      902
Gly Thr His Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln
            225              230              235

gag cct cag ctt gtc cct gaa ggc tgc caa gaa cct gag gag ata agc      950
Glu Pro Gln Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser
            240              245              250

tgg cct cca tca gtg gag acc agt gtc tcc tta ggg tta cca cac gaa      998
Trp Pro Pro Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu
            255              260              265

att agc gtt cca gag gtg tct cca gag gag gct tcg ccc atc ctc cct     1046
Ile Ser Val Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro
270              275              280              285

gac gcc ctg gct gct cca gac aca agt gtc cac tgt ccc att gaa tgc     1094
Asp Ala Leu Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys
            290              295              300

aca gag ttg tct aca aac tcc agg tct ccc ctg acg tcc acc aca gaa     1142
Thr Glu Leu Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu
            305              310              315

agt gtt gga aag cag tgg cct att aca agt cag agg tca cct cag gtt     1190
Ser Val Gly Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val
            320              325              330

cct gta gga gat gat tct ctg cag aac acc acg tca tcc agc cct cct     1238
Pro Val Gly Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro
            335              340              345

gcc cag cca cca tcc ctc caa gcc tcc cct aag ctg cct cct tcc cct     1286
Ala Gln Pro Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro
350              355              360              365

ctg tcc tct gct tcc tcc ccg agc agc tac cct gct cct cca acc tcc     1334
Leu Ser Ser Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser
            370              375              380

aca tcc cct gtt ttg gac cac tca gaa aca tct gat cag aaa ttc tat     1382
Thr Ser Pro Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr
            385              390              395

aac ttt gtg gtt atc cat gcc agg gct gat gaa cag gtg gcc cta cgt     1430
Asn Phe Val Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg
            400              405              410

att cgg gag aag ctg gag acc ctc ggg gta cct gac ggg gcc acc ttc     1478
Ile Arg Glu Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe
```

280

```
tgt gag gaa ttt cag gtg ccc ggg cgt ggt gag ctg cac tgt ctc caa    1526
Cys Glu Glu Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln
430             435             440             445

gat gcc atc gat cac tcg ggg ttc acg atc ctg ctc ctg act gct agc    1574
Asp Ala Ile Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser
                450             455             460

ttt gat tgc agc ctg agc ctg cat caa atc aac cat gct ctc atg aac    1622
Phe Asp Cys Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn
            465             470             475

agc ctt aca cag tct ggg agg cag gac tgt gtg atc ccc ctc ctc cca    1670
Ser Leu Thr Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro
            480             485             490

ctt gag tgt tcc cag gcc cag ctc agc cca gat aca acc aga ctg ctc    1718
Leu Glu Cys Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu
        495             500             505

cac agc att gtg tgg ctg gat gaa cac tcc cca atc ttc gcc aga aag    1766
His Ser Ile Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys
510             515             520             525

gtg gca aac acc ttc aag aca cag aag ctc cag gca cag cgg gta cgc    1814
Val Ala Asn Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg
                530             535             540

tgg aag aaa gcg cag gag gcc aga acc ctc aag gag cag agc ata cag    1862
Trp Lys Lys Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln
            545             550             555

ctg gag gca gag cgg caa aac gtg gca gcc ata tct gct gcc tac aca    1910
Leu Glu Ala Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr
            560             565             570

gcc tat gtc cat agc tat agg gcc tgg caa gca gag atg aac aaa ctt    1958
Ala Tyr Val His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu
        575             580             585

ggg gtg gct ttt ggg aag aac ttg tca ctg ggg act cca aca ccc agc    2006
Gly Val Ala Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser
590             595             600             605

tgg ccc gga tgt cca cag cca ata cct tct cat cct cag ggt ggt act    2054
Trp Pro Gly Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr
            610             615             620

cca gtt ttc ccc tat tcc cca cag cct cca tcc ttc cct cag cct cca    2102
Pro Val Phe Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro
            625             630             635

tgc ttc cct cag cct cca tcc ttc cct cag cct cca tcc ttc cca ctg    2150
Cys Phe Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu
            640             645             650
```

```
cct cca gtc tct tcc cca cag tcc caa tcc ttt cca tca gcc tcc tcc   2198
Pro Pro Val Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser
    655                 660                 665

cca gcc cca cag act cca gga cct cag cct ctc att att cac cat gcc   2246
Pro Ala Pro Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala
670                 675                 680                 685

cag atg gtt cag ctg ggt gtc aac aat cac atg tgg ggc cac aca ggg   2294
Gln Met Val Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly
                690                 695                 700

gcc cag tca tct gat gac aag act gag tgt tcg gag aac ccc tgt atg   2342
Ala Gln Ser Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met
            705                 710                 715

ggc cct ctg act gat cag ggc gaa ccc ctt ctt gag act cca gag       2387
Gly Pro Leu Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu
        720                 725                 730

tgaccaggtt ggaccccacc tagatggcta gagtgacaag attggacttc acctgggtcc   2447

ttaaaatgat agtggaggaa gggaacctcg cctgggtccc cagagtagcc agaggactta   2507

gcttgggctc ccacagtggc tattagttgg acccagcttg agaccccaga ggcagggaag   2567

accacaccta taaatcaggc ctgggaaaca tgcagaaacc ccatttgaac agactgtggg   2627

actccaatct gaatcctcta tgtggacaga ggatgatggg gccagaggca cctctgaggt   2687

gccctcagcg cagcctcgta aacttcattc actgtgacac atgctgttca tagggtctct   2747

ctggggagga tgcggtcccg gggcacatag ggagggtcct gtttttataa taaagttatt   2807

gacaactg                                                           2815


<210> 152
<211> 732
<212> PRT
<213> Mus musculus

<400> 152
Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly Ile Leu Gly
 1               5                  10                  15

Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys Leu Gly Ser
            20                  25                  30

Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val Leu
        35                  40                  45

Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser Leu
    50                  55                  60

Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp Ala Asp Met
```

282

Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser Trp Thr Val
                85   90   95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys Pro Ala Ser
                100   105   110

Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe Ala Ser Gln
                115   120   125

Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp Asp Arg Cys
        130   135   140

Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro Leu His Ser
145   150   155   160

His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala Val Thr Arg
                165   170   175

Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp Gly His Thr
                180   185   190

Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His Leu Glu Ile
                195   200   205

Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His Gly Thr His
        210   215   220

Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln Glu Pro Gln
225   230   235   240

Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser Trp Pro Pro
                245   250   255

Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu Ile Ser Val
                260   265   270

Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro Asp Ala Leu
                275   280   285

Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys Thr Glu Leu
        290   295   300

Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu Ser Val Gly
305   310   315   320

Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val Pro Val Gly
                325   330   335

Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro Ala Gln Pro
        340   345   350

Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro Leu Ser Ser
        355   360   365

Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser Thr Ser Pro

283

Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr Asn Phe Val
385   390   395   400

Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg Ile Arg Glu
                405   410   415

Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Glu
                420   425   430

Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln Asp Ala Ile
                435   440   445

Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser Phe Asp Cys
                450   455   460

Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn Ser Leu Thr
465   470   475   480

Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro Leu Glu Cys
                485   490   495

Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu His Ser Ile
                500   505   510

Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys Val Ala Asn
                515   520   525

Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg Trp Lys Lys
                530   535   540

Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln Leu Glu Ala
545   550   555   560

Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr Ala Tyr Val
                565   570   575

His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu Gly Val Ala
                580   585   590

Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser Trp Pro Gly
                595   600   605

Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr Pro Val Phe
                610   615   620

Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Cys Phe Pro
625   630   635   640

Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu Pro Pro Val
                645   650   655

Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser Pro Ala Pro
                660   665   670

Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala Gln Met Val

```
Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly Ala Gln Ser
    690             695             700

Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met Gly Pro Leu
705             710             715             720

Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu
                725             730
```

<210> 153
<211> 2544
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (97)..(2232)

<400> 153

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taggggacac tgggcgtgca gaaggcgggg ggcagtgtgg aacatgcctt caccacctcc   60

agcttctgct gccggaggct gcacccacct gtgccc atg gcc tgc aca ggc cca   114
                                        Met Ala Cys Thr Gly Pro
                                          1               5

tca ctt cct agc gcc ttc gac att cta ggt gca gca ggc cag gac aag   162
Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly Ala Ala Gly Gln Asp Lys
            10              15                  20

ctc ttg tat ctg aag cac aaa ctg aag acc cca cgc cca ggc tgc cag   210
Leu Leu Tyr Leu Lys His Lys Leu Lys Thr Pro Arg Pro Gly Cys Gln
        25              30                  35

ggg cag gac ctc ctg cat gcc atg gtt ctc ctg aag ctg ggc cag gaa   258
Gly Gln Asp Leu Leu His Ala Met Val Leu Leu Lys Leu Gly Gln Glu
    40              45                  50

act gag gcc agg atc tct cta gag gca ttg aag gcc gat gcg gtg gcc   306
Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu Lys Ala Asp Ala Val Ala
 55                 60                  65                  70

cgg ctg gtg gcc cgc cag tgg gct ggc gtg gac agc acc gag gac cca   354
Arg Leu Val Ala Arg Gln Trp Ala Gly Val Asp Ser Thr Glu Asp Pro
                75                  80                  85

gag gag ccc cca gat gtg tcc tgg gct gtg gcc cgc ttg tac cac ctg   402
Glu Glu Pro Pro Asp Val Ser Trp Ala Val Ala Arg Leu Tyr His Leu
                90                  95                  100

ctg gct gag gag aag ctg tgc ccc gcc tcg ctg cgg gac gtg gcc tac   450
Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser Leu Arg Asp Val Ala Tyr
        105             110                 115

cag gaa gcc gtc cgc acc ctc agc tcc agg gac gac cac cgg ctg ggg   498
Gln Glu Ala Val Arg Thr Leu Ser Ser Arg Asp Asp His Arg Leu Gly
```

285

```
        Gln Glu Ala Val Arg Thr Leu Ser Ser Arg Asp Asp His Arg Leu Gly
            120                 125                 130

gaa ctt cag gat gag gcc cga aac cgg tgt ggg tgg gac att gct ggg      546
Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys Gly Trp Asp Ile Ala Gly
135                 140                 145                 150

gat cca ggg agc atc cgg acg ctc cag tcc aat ctg ggc tgc ctc cca      594
Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser Asn Leu Gly Cys Leu Pro
                    155                 160                 165

cca tcc tcg gct ttg ccc tct ggg acc agg agc ctc cca cgc ccc att      642
Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg Ser Leu Pro Arg Pro Ile
                170                 175                 180

gac ggt gtt tcg gac tgg agc caa ggg tgc tcc ctg cga tcc act ggc      690
Asp Gly Val Ser Asp Trp Ser Gln Gly Cys Ser Leu Arg Ser Thr Gly
            185                 190                 195

agc cct gcc tcc ctg gcc agc aac ttg gaa atc agc cag tcc cct acc      738
Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu Ile Ser Gln Ser Pro Thr
        200                 205                 210

atg ccc ttc ctc agc ctg cac cgc agc cca cat ggg ccc agc aag ctc      786
Met Pro Phe Leu Ser Leu His Arg Ser Pro His Gly Pro Ser Lys Leu
215                 220                 225                 230

tgt gac gac ccc cag gcc agc ttg gtg ccc gag cct gtc ccc ggt ggc      834
Cys Asp Asp Pro Gln Ala Ser Leu Val Pro Glu Pro Val Pro Gly Gly
                235                 240                 245

tgc cag gag cct gag gag atg agc tgg ccg cca tcg ggg gag att gcc      882
Cys Gln Glu Pro Glu Glu Met Ser Trp Pro Pro Ser Gly Glu Ile Ala
                250                 255                 260

agc cca cca gag ctg cca agc agc cca cct cct ggg ctt ccc gaa gtg      930
Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro Pro Gly Leu Pro Glu Val
            265                 270                 275

gcc cca gat gca acc tcc act ggc ctc cct gat acc ccc gca gct cca      978
Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro Asp Thr Pro Ala Ala Pro
            280                 285                 290

gaa acc agc acc aac tac cca gtg gag tgc acc gag ggg tct gca ggc     1026
Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys Thr Glu Gly Ser Ala Gly
295                 300                 305                 310

ccc cag tct ctc ccc ttg cct att ctg gag ccg gtc aaa aac ccc tgc     1074
Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu Pro Val Lys Asn Pro Cys
                315                 320                 325

tct gtc aaa gac cag acg cca ctc caa ctt tct gta gaa gat acc acc     1122
Ser Val Lys Asp Gln Thr Pro Leu Gln Leu Ser Val Glu Asp Thr Thr
                330                 335                 340

tct cca aat acc aag ccg tgc cca cct act ccc acc acc cca gaa aca     1170
Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr Pro Thr Thr Pro Glu Thr
```

286

```
tcc cct cct cct cct cct cct cct cct tca tct act cct tgt tca gct   1218
Ser Pro Pro Pro Pro Pro Pro Pro Ser Ser Thr Pro Cys Ser Ala
    360             365             370

cac ctg acc ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tcg   1266
His Leu Thr Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser
375             380             385             390

gaa cag aaa ttc tat aac ttt gtg atc ctc cac gcc agg gca gac gaa   1314
Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu
                395             400             405

cac atc gcc ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc   1362
His Ile Ala Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro
            410             415             420

gac ggg gcc acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag   1410
Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu
            425             430             435

ctg agc tgc ctg cag gac gcc ata gac cac tca gct ttc atc atc cta   1458
Leu Ser Cys Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu
    440             445             450

ctt ctc acc tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac   1506
Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn
455             460             465             470

caa gcc atg atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc   1554
Gln Ala Met Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val
                475             480             485

atc ccc ttc ctg ccc ctg gag agc tcc ccg gcc cag ctc agc tcc gac   1602
Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro Ala Gln Leu Ser Ser Asp
            490             495             500

acg gcc agc ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag   1650
Thr Ala Ser Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln
    505             510             515

atc ttc gcc agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag   1698
Ile Phe Ala Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln
    520             525             530

gcc cga aag gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg   1746
Ala Arg Lys Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg
535             540             545             550

gaa cag agc caa cac ctg gac ggt gag cgg atg cag gcg gcg gca ctg   1794
Glu Gln Ser Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu
                555             560             565

aac gca gcc tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca   1842
Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala
            570             575             580
```

287

```
cag atg gag cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg       1890
Gln Met Glu Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly
        585                 590                 595

act ggg gcg ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc       1938
Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro
        600                 605                 610

ctg gga gcc ccg cca ccc ttt ccc act tgg ccg ggg tgc ccg cag ccg       1986
Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro
615                 620                 625                 630

cca ccc ctg cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca       2034
Pro Pro Leu His Ala Trp Gln Ala Gly Thr Pro Pro Pro Pro Ser Pro
                635                 640                 645

cag cca gca gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc       2082
Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala
                650                 655                 660

ttc cct acg gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc       2130
Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro
                665                 670                 675

ctc att atc cac cac gca cag atg gta cag ctg ggg ctg aac aac cac       2178
Leu Ile Ile His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His
        680                 685                 690

atg tgg aac cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag       2226
Met Trp Asn Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu
695                 700                 705                 710

gca gaa tgaccgcgtg tccttgcctg accacctggg aacacccct ggacccaggc        2282
Ala Glu

atcggccagg accccataga gcaccccggt ctgccctgtg ccctgtggac agtggaagat    2342

gaggtcatct gccactttca ggacattgtc cgggagccct tcatttagga caaaacgggc    2402

gcgatgatgc cctggctttc agggtggtca gaactggata cggtgtttac aattccaatc    2462

tctctatttc tgggtgaagg gtcttggtgg tgggggtatt gctacggtct tttaattata    2522

ataaatattt attgaatgct tc                                             2544


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<212> PRT
<213> Homo sapiens

<400> 154
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  1               5                  10                  15

Ala Ala Gly Gln Asp Lys Leu Leu Tyr Leu Lys His Lys Leu Lys Thr
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288

Pro Arg Pro Gly Cys Gln Gly Gln Asp Leu Leu His Ala Met Val Leu
        35   40   45

Leu Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu
        50   55   60

Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val
65   70   75   80

Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala Val
                85   90   95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser
        100   105   110

Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser Arg
        115   120   125

Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys
        130   135   140

Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser
145   150   155   160

Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg
        165   170   175

Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys
        180   185   190

Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu
        195   200   205

Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser Pro
        210   215   220

His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val Pro
225   230   235   240

Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp Pro
                245   250   255

Pro Ser Gly Glu Ile Ala Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro
                260   265   270

Pro Gly Leu Pro Glu Val Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro
        275   280   285

Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys
        290   295   300

Thr Glu Gly Ser Ala Gly Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu
305   310   315   320

Pro Val Lys Asn Pro Cys Ser Val Lys Asp Gln Thr Pro Leu Gln Leu

Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr
        340   345   350

Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Pro Ser
        355   360   365

Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro Ser
        370   375   380

Ser Leu Glu Ser Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu
385   390   395   400

His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys Leu
                405   410   415

Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln
        420   425   430

Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp His
        435   440   445

Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu
        450   455   460

Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg Gln
465   470   475   480

Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro
                485   490   495

Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val Arg
            500   505   510

Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr Phe
        515   520   525

Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu Gln
        530   535   540

Asp Thr Arg Ala Leu Arg Glu Gln Ser Gln His Leu Asp Gly Glu Arg
545   550   555   560

Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser
            565   570   575

Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly
            580   585   590

Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro
        595   600   605

Phe Gly Gly Gln Val Pro Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp
        610   615   620

Pro Gly Cys Pro Gln Pro Pro Pro Leu His Ala Trp Gln Ala Gly Thr

290

```
Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro
                 645             650                 655

Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln
                 660             665                 670

Ser Pro Gly Leu Gln Pro Leu Ile Ile His His Ala Gln Met Val Gln
                 675             680                 685

Leu Gly Leu Asn Asn His Met Trp Asn Gln Arg Gly Ser Gln Ala Pro
         690             695             700

Glu Asp Lys Thr Gln Glu Ala Glu
705                 710
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<211> 3456
<212> DNA
<213> Homo sapiens

<220>
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<222> (281)..(3016)

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cgtgtccacc cggtcatgcc cgccgcgcac cagccccgca gtggacttgg aggaggagga 120

ggaggagagc tctgtggatg gcaaaggga ccggaagagc acaggcctga aactctccaa 180

gaagaaagca aggaggagac acacggatga cccaagcaag gaatgcttca ctctgaaatt 240

tgacctgaat gtggacattg agacagagat cgtcccagcc atg aag aag aag tca   295
                                             Met Lys Lys Lys Ser
                                              1               5

ctg ggg gag gtg ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg   343
Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu
                10              15                  20

ggc aaa gtg gac atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc   391
Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu
            25                  30                  35

acc ttc gag gcc tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc   439
Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala
        40                  45                  50

cca gcc aag cct gga gat gag ggc aag gtg gag cag ggc atg aag gac   487
Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp
    55                  60                  65

tcc aag tcc ctg agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc   535
```

291

```
ccc gcc ctg gag cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac   583
Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp
             90              95              100

atc ttg gcc cct ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg   631
Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly
             105             110             115

gag gcg agc atc ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct   679
Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser
             120             125             130

ctg ccc agc ggc agc agt ggc agc acc aac act ggc gac agc tgg aag   727
Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys
         135             140             145

aac cgg gcg gcc agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc   775
Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser
150             155             160             165

acc agc gcc ttt ggc cgg gag gta gac aag atg gag cag ctg gag ggc   823
Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly
             170             175             180

aag ctg cac acc tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg   871
Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly
             185             190             195

ctg cgc ttc gac cat gac tcc tgg gag gag gag tac gat gaa gac gag   919
Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu
         200             205             210

gat gag gac aat gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc   967
Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu
         215             220             225

att gat ggg cat gag aag ctg acc cgg cgg cag tgc cac cag cag gag   1015
Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu
230             235             240             245

gcg gtg tgg gag ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg   1063
Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu
             250             255             260

cgg gtg atc atc aac ctg ttc ttg tgc tgc ctc ctg aac ctg caa gag   1111
Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu
             265             270             275

tca ggg ctg ctg tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc   1159
Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile
         280             285             290

ccg gag atc gcg cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg   1207
Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala
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ccg gtg ctg gag aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg   1255
Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly
310   315   320   325

gac ttc ctc aaa ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac   1303
Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr
                  330   335   340

atc cgc tac tgc atg gag gag gag ggc tgc atg gag tac atg cgc ggc   1351
Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly
                  345   350   355

ctg ctg cgc gac aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag   1399
Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu
              360   365   370

aag cac cca cag tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa   1447
Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys
              375   380   385

ccc cac cag cgg ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg   1495
Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu
390   395   400   405

agg aag acc gag gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc   1543
Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile
              410   415   420

ggc tcc gtg gag cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag   1591
Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln
              425   430   435

cgg cag gag cgg cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc   1639
Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala
              440   445   450

tac gag gtg gtg gaa agc agc agc gac gaa gtg gac aag ctc ctg aag   1687
Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys
              455   460   465

gaa ttt ctg cac ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg   1735
Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro
470   475   480   485

gag gag acg cgg cag ctg ctg ctg gag ggg agc ctg agg atg aag gag   1783
Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu
              490   495   500

ggg aag gac agc aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg   1831
Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu
              505   510   515

ctg ttg gtg acc aaa gca gtg aag aag gca gag agg acc agg gtc atc   1879
Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile
              520   525   530

293

```
agg cca ccc ctg ctc gtg gac aag att gtg tgc cgg gag cta cgg gac   1927
Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp
    535                 540                 545

cct ggg tcc ttc ctc ctt atc tac ctg aat gag ttt cac agt gct gta   1975
Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val
550                 555                 560                 565

ggg gcc tac acg ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg   2023
Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp
                570                 575                 580

gtg gac acc att tac aat gcc cag aac cag ctg caa cag ctg cgt gca   2071
Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala
                585                 590                 595

cag gag ccc cca ggc agt cag cag ccc ctg cag agc ctg gaa gag gag   2119
Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu
        600                 605                 610

gag gat gag cag gag gag gaa gag gag gag gag gag gag gag gag gaa   2167
Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
        615                 620                 625

ggc gag gac agt ggc act tca gct gcc agc tcc cct acc atc atg cgg   2215
Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg
630                 635                 640                 645

aaa agc agc ggc agc ccc gac tct cag cac tgt gcc tca gat ggc tcc   2263
Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser
                650                 655                 660

acg gag acc ctg gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc   2311
Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser
                665                 670                 675

tcc ccc gag ttc gac agc ggt cct ttc agc tcc cag tct gat gag acc   2359
Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr
        680                 685                 690

tct ctc agc acc act gcc tca tct gcc acg ccc acc agt gag ctg ctg   2407
Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu
    695                 700                 705

ccc ctg ggt ccg gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac   2455
Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr
710                 715                 720                 725

ggc acc ctc tcc cca acc tcc tta caa gac ttt gtg gcc cca ggc cca   2503
Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro
                730                 735                 740

atg gca gag cta gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc   2551
Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser
            745                 750                 755
```

294

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cct cca ccc tcg ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg    2599
Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu
        760                 765             770

agc tgc ccg ccc cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc    2647
Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu
        775             780             785

cag ctg ctg gca ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc    2695
Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser
790             795             800             805

cgc agc ctg tca gag ctc tgc ctg gct gtt cca gcc cca ggt att agg    2743
Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg
            810             815             820

act cag ggc tcc cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg    2791
Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly
            825             830             835

gcc cct agc cct ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg    2839
Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly
        840             845             850

gaa cct gca ggc tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg    2887
Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly
        855             860             865

gcc tct ccc agg gtc cag cct gag ccc cca cca ggg gtc tct gcc cag    2935
Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln
870             875             880             885

cac agg aag ctg acc ctg gcc cag ctc tac cga atc agg acc acc ctg    2983
His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu
                890             895             900

ctg ctt aac tcc acg ctc act gcc tcg gag gtc tgagcagagg gaggcccca   3036
Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val
                905             910

agagtgccat tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc   3096

ttcagctact gcctcctgta tgcatgagcc ggatgctggg caggatccct gcctacgccc   3156

gggcccgatt tgcgctttgc cggactggat ggagtggagg aggcccaggc cacagtacca   3216

ccccacctgc ccaggcagcc cctcgtcacc tactccccga agttaccagc tcagctcgag   3276

tcttcagggc tgggctccta ggctgcccat cctacttcta ccctcactgg cctccagtgg   3336

gattcactcc tgccctgccc ccaccttccc agtcccacag gccacccctg gcttgggctg   3396

ggttctgtga agttacgtat ttattgagct tttggttctt ttataaagac ttgtctagac   3456
```

<210> 156
<211> 912

295

<212> PRT
<213> Homo sapiens

<400> 156
Met Lys Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg
1   5   10   15

Lys Gly Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn
            20   25   30

Thr Pro Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr
            35   40   45

Leu Arg Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu
        50   55   60

Gln Gly Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro
65   70   75   80

Ala Gly Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg
                85   90   95

Arg Glu Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met
            100   105   110

Ser Glu Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr
            115   120   125

Pro Ser Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr
        130   135   140

Gly Asp Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe
145   150   155   160

Ser Ser Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met
                165   170   175

Glu Gln Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro
            180   185   190

Arg Leu Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu
        195   200   205

Tyr Asp Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp
    210   215   220

Ser Trp Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln
225   230   235   240

Cys His Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser
                245   250   255

Tyr Ile Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu
            260   265   270

Leu Asn Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg
        275   280   285

296

```
Leu Phe Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp
    290             295             300

Ala Ser Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala
305             310             315             320

Leu Leu Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser
            325             330             335

Leu Phe Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met
            340             345             350

Glu Tyr Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr
        355             360             365

Ile Thr Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser
    370             375             380

Asp Met Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu
385             390             395             400

Leu Lys Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala
            405             410             415

Val Val Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn
            420             425             430

Ala Cys Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val
            435             440             445

Ser Arg Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val
    450             455             460

Asp Lys Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile
465             470             475             480

Pro Gly Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser
            485             490             495

Leu Arg Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe
        500             505             510

Leu Phe Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu
        515             520             525

Arg Thr Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys
        530             535             540

Arg Glu Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu
545             550             555             560

Phe His Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala
            565             570             575

Leu Cys Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu
            580             585             590
```

297

```
Gln Gln Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln
        595                 600                 605

Ser Leu Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu
        610                 615                 620

Glu Glu Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser
625                 630                 635                 640

Pro Thr Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys
                645                 650                 655

Ala Ser Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro
                660                 665                 670

Gly Asp Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser
            675                 680                 685

Gln Ser Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro
    690                 695                 700

Thr Ser Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser
705                 710                 715                 720

Met Asp Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe
                725                 730                 735

Val Ala Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser
            740                 745                 750

Pro Arg Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr
        755                 760                 765

Pro Val Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser
    770                 775                 780

Glu Ala Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr
785                 790                 795                 800

Pro Ser Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro
            805                 810                 815

Ala Pro Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser
            820                 825                 830

Trp Asp Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val
        835                 840                 845

Gly Cys Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly
    850                 855                 860

Asp Leu Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro
865                 870                 875                 880

Gly Val Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg
                885                 890                 895
```

298

```
        Ile Arg Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val
                    900                 905                 910


<210> 157
<211> 3609
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (152)..(3169)

<400> 157
agatgaagac cagggagagg aaagggtgga cctgaggccc ccatggagaa gggacgggca   60

ggatgtatgt caccacgccg actgccagca gctgcaccgc cgggggcccc tcaacctctg  120

cgaggcctgt gacagcaagt tccacagcac c atg cat tat gat ggg cat gtc      172
                                    Met His Tyr Asp Gly His Val
                                     1               5

cgc ttc gac ctt ccc cca caa ggc tct gtg ctg gcc cgg aac gtg tcc    220
Arg Phe Asp Leu Pro Pro Gln Gly Ser Val Leu Ala Arg Asn Val Ser
             10              15              20

acc cgg tca tgc ccg ccg cgc acc agc ccc gca gtg gac ttg gag gag    268
Thr Arg Ser Cys Pro Pro Arg Thr Ser Pro Ala Val Asp Leu Glu Glu
     25              30              35

gag gag gag gag agc tct gtg gat ggc aaa ggg gac cgg aag agc aca    316
Glu Glu Glu Glu Ser Ser Val Asp Gly Lys Gly Asp Arg Lys Ser Thr
 40              45              50                      55

ggc ctg aaa ctc tcc aag aag aaa gca agg agg aga cac acg gat gac    364
Gly Leu Lys Leu Ser Lys Lys Lys Ala Arg Arg Arg His Thr Asp Asp
                 60              65              70

cca agc aag gaa tgc ttc act ctg aaa ttt gac ctg aat gtg gac att    412
Pro Ser Lys Glu Cys Phe Thr Leu Lys Phe Asp Leu Asn Val Asp Ile
                 75              80              85

gag aca gag atc gtc cca gcc atg aag aag aag tca ctg ggg gag gtg    460
Glu Thr Glu Ile Val Pro Ala Met Lys Lys Lys Ser Leu Gly Glu Val
             90              95             100

ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg ggc aaa gtg gac    508
Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu Gly Lys Val Asp
    105             110             115

atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc acc ttc gag gcc    556
Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu Thr Phe Glu Ala
120             125             130             135

tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc cca gcc aag cct    604
Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala Pro Ala Lys Pro
```

299

gga gat gag ggc aag gtg gag cag ggc atg aag gac tcc aag tcc ctg   652
Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp Ser Lys Ser Leu
            155   160   165

agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc ccc gcc ctg gag   700
Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro Pro Ala Leu Glu
            170   175   180

cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac atc ttg gcc cct   748
Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp Ile Leu Ala Pro
            185   190   195

ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg gag gcg agc atc   796
Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly Glu Ala Ser Ile
200   205   210   215

ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct ctg ccc agc ggc   844
Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser Leu Pro Ser Gly
                220   225   230

agc agt ggc agc acc aac act ggc gac agc tgg aag aac cgg gcg gcc   892
Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys Asn Arg Ala Ala
            235   240   245

agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc acc agc gcc ttt   940
Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser Thr Ser Ala Phe
            250   255   260

ggc cgg gag gta gac aag atg gag cag ctg gag ggc aag ctg cac acc   988
Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly Lys Leu His Thr
            265   270   275

tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg ctg cgc ttc gac   1036
Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly Leu Arg Phe Asp
280   285   290   295

cat gac tcc tgg gag gag gag tac gat gaa gac gag gat gag gac aat   1084
His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu Asp Glu Asp Asn
                300   305   310

gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc att gat ggg cat   1132
Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu Ile Asp Gly His
            315   320   325

gag aag ctg acc cgg cgg cag tgc cac cag cag gag gcg gtg tgg gag   1180
Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu Ala Val Trp Glu
            330   335   340

ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg cgg gtg atc atc   1228
Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu Arg Val Ile Ile
            345   350   355

aac ctg ttc ctg tgc tgc ctc ctg aac ctg caa gag tca ggg ctg ctg   1276
Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu Ser Gly Leu Leu
360   365   370   375

300

tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc ccg gag atc gcg   1324
Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile Pro Glu Ile Ala
                380   385   390

cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg ccg gtg ctg gag   1372
Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala Pro Val Leu Glu
                395   400   405

aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg gac ttc ctc aaa   1420
Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly Asp Phe Leu Lys
                410   415   420

ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac atc cgc tac tgc   1468
Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr Ile Arg Tyr Cys
            425   430   435

atg gag gag gag ggc tgc atg gag tac atg cgc ggc ctg ctg cgc gac   1516
Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly Leu Leu Arg Asp
440   445   450   455

aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag aag cac cca cag   1564
Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu Lys His Pro Gln
                460   465   470

tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa ccc cac cag cgg   1612
Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys Pro His Gln Arg
                475   480   485

ctc acc aag tac ccg ctg ctc ctc aag tcg gtg ctg agg aag acc gag   1660
Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu Arg Lys Thr Glu
                490   495   500

gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc ggc tcc gtg gag   1708
Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile Gly Ser Val Glu
        505   510   515

cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag cgg cag gag cgg   1756
Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln Arg Gln Glu Arg
520   525   530   535

cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc tac gag gtg gtg   1804
Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala Tyr Glu Val Val
                540   545   550

gaa agc agc agc gac gaa gtg gac aag ctc ctg aag gaa ttt ctg cac   1852
Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys Glu Phe Leu His
                555   560   565

ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg gag gag acg cgg   1900
Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro Glu Glu Thr Arg
                570   575   580

cag ctg ctg ctg gag ggg agc ctg agg atg aag gag ggg aag gac agc   1948
Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu Gly Lys Asp Ser
        585   590   595

301

```
_aag atg_gat gtg tac_tgc ttc ctc_ttc acg_gat ctg ctg_ttg gtg acc  —1996 —
Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu Leu Leu Val Thr
600             605             610             615

aaa gca gtg aag aag gca gag agg acc agg gtc atc agg cca ccc ctg    2044
Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile Arg Pro Pro Leu
                620             625             630

ctc gtg gac aag att gtg tgc cgg gag cta cgg gac cct ggg tcc ttc    2092
Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp Pro Gly Ser Phe
                635             640             645

ctc ctt atc tac ctg aat gag ttt cac agt gct gta ggg gcc tac acg    2140
Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val Gly Ala Tyr Thr
                650             655             660

ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg gtg gac acc att    2188
Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp Val Asp Thr Ile
    665             670             675

tac aat gcc cag aac cag ctg caa cag ctg cgt gca cag gag ccc cca    2236
Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala Gln Glu Pro Pro
680             685             690             695

ggc agt cag cag ccc ctg cag agc ctg gaa gag gag gag gat gag cag    2284
Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu Glu Asp Glu Gln
                700             705             710

gag gag gaa gag gag gag gag gag gag gag gag gaa ggc gag gac agt    2332
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Glu Asp Ser
                715             720             725

ggc act tca gct gcc agc tcc cct acc atc atg cgg aaa agc agc ggc    2380
Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg Lys Ser Ser Gly
        730             735             740

agc ccc gac tct cag cac tgt gcc tca gat ggc tcc acg gag acc ctg    2428
Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser Thr Glu Thr Leu
    745             750             755

gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc tcc ccc gag ttc    2476
Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser Ser Pro Glu Phe
760             765             770             775

gac agc ggt cct ttc agc tcc cag tct gat gag acc tct ctc agc acc    2524
Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr Ser Leu Ser Thr
                780             785             790

act gcc tca tct gcc acg ccc acc agt gag ctg ctg ccc ctg ggt ccg    2572
Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu Pro Leu Gly Pro
            795             800             805

gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac ggc acc ctc tcc    2620
Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr Gly Thr Leu Ser
            810             815             820

cca acc tcc tta caa gac ttt gtg gcc cca ggc cca atg gca gag cta    2668
```

302

```
Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro Met Ala Glu Leu
    825                 830                 835

gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc cct cca ccc tcg   2716
Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser Pro Pro Pro Ser
840                 845                 850                 855

ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg agc tgc ccg ccc   2764
Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu Ser Cys Pro Pro
                860                 865                 870

cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc cag ctg ctg gca   2812
His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu Gln Leu Leu Ala
                875                 880                 885

ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc cgc agc ctg tca   2860
Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser Arg Ser Leu Ser
            890                 895                 900

gag ctc tgc ctg gct gtt cca gcc cca ggt att agg act cag ggc tcc   2908
Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg Thr Gln Gly Ser
    905                 910                 915

cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg gcc cct agc cct   2956
Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly Ala Pro Ser Pro
920                 925                 930                 935

ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg gaa cct gca ggc   3004
Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly Glu Pro Ala Gly
                940                 945                 950

tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg gcc tct ccc agg   3052
Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly Ala Ser Pro Arg
                955                 960                 965

gtc cag cct gag ccc cca cca ggg gtc tct gcc cag cac agg aag ctg   3100
Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln His Arg Lys Leu
            970                 975                 980

acc ctg gcc cag ctc tac cga atc agg acc acc ctg ctg ctt aac tcc   3148
Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu Leu Leu Asn Ser
    985                 990                 995

acg ctc act gcc tcg gag gtc tgagcagagg gaggccccca agagtgccat       3199
Thr Leu Thr Ala Ser Glu Val
1000                1005

tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc ttcagctact   3259

gcctcctgta tgcatgagcc ggatgctggg caggatccct gcctacgccc gggcccgatt   3319

tgcgctttgc cggactggat ggagtggagg aggcccaggc acagtacca ccccacctgc    3379

ccaggcagcc cctcgtcacc tactccccga agttaccagc tcagctcgag tcttcagggc   3439

tgggctccta ggctgcccat cctacttcta ccctcactgg cctccagtgg gattcactcc   3499
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303

tgccctgccc ccacctccc agtcccacag gccacccctg gcttgggctg ggttctgtga 3559

agttacgtat ttattgagct tttggttctt ttataaagac ttgtctagac   3609

<210> 158
<211> 1006
<212> PRT
<213> Homo sapiens

<400> 158
Met His Tyr Asp Gly His Val Arg Phe Asp Leu Pro Pro Gln Gly Ser
 1   5   10   15

Val Leu Ala Arg Asn Val Ser Thr Arg Ser Cys Pro Pro Arg Thr Ser
            20   25   30

Pro Ala Val Asp Leu Glu Glu Glu Glu Glu Ser Ser Val Asp Gly
        35   40   45

Lys Gly Asp Arg Lys Ser Thr Gly Leu Lys Leu Ser Lys Lys Lys Ala
    50   55   60

Arg Arg Arg His Thr Asp Asp Pro Ser Lys Glu Cys Phe Thr Leu Lys
65   70   75   80

Phe Asp Leu Asn Val Asp Ile Glu Thr Glu Ile Val Pro Ala Met Lys
                85   90   95

Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly
            100   105   110

Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro
        115   120   125

Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg
    130   135   140

Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly
145   150   155   160

Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly
                165   170   175

Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu
                180   185   190

Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu
            195   200   205

Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser
    210   215   220

Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp
225   230   235   240

Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser

304

Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln
        260   265   270

Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu
        275   280   285

Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp
        290   295   300

Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp
305   310   315   320

Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His
        325   330   335

Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile
        340   345   350

Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn
        355   360   365

Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe
        370   375   380

Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser
385   390   395   400

Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu
        405   410   415

Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe
        420   425   430

Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr
        435   440   445

Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr
        450   455   460

Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met
465   470   475   480

Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys
        485   490   495

Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val
        500   505   510

Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys
        515   520   525

Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg
        530   535   540

Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys

305

Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly
            565   570   575

Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg
            580   585   590

Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe
            595   600   605

Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr
610   615   620

Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu
625   630   635   640

Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His
            645   650   655

Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys
            660   665   670

Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln
            675   680   685

Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu
            690   695   700

Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu
705   710   715   720

Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr
            725   730   735

Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser
            740   745   750

Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp
            755   760   765

Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser
            770   775   780

Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser
785   790   795   800

Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp
            805   810   815

Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala
            820   825   830

Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg
            835   840   845

Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val

306

```
Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala
865             870             875             880

Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser
            885             890             895

Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro
            900             905             910

Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp
            915             920             925

Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys
        930             935             940

Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu
945             950             955             960

Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val
            965             970             975

Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg
            980             985             990

Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val
        995             1000            1005
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<210> 159
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<213> Homo sapiens

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<222> (93)..(3089)

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cactggcgcg atgcgggccg tcctctcggc tg atg ggt tgg aag ccc agc gag   113
                                     Met Gly Trp Lys Pro Ser Glu
                                      1               5

gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg   161
Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg
        10              15              20

agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga   209
Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg
    25              30              35

gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg   257
Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val
 40              45              50              55
```

```
ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac   305
Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp
                60                  65              70

ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc   353
Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly
            75                  80              85

agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc   401
Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly
        90                  95              100

acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg   449
Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu
    105                 110             115

ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt   497
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys
120                 125             130             135

gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt   545
Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg
                140             145             150

gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag   593
Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys
            155             160             165

cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc   641
His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg
            170             175             180

cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg   689
Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg
    185                 190             195

ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg   737
Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp
200                 205             210             215

ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc   785
Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile
                220             225             230

cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg   833
Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp
            235             240             245

gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg   881
Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val
            250             255             260

gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac   929
Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp
    265                 270             275
```

308

```
cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt    977
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser
280                 285                 290                 295

gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg    1025
Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu
                    300                 305                 310

gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac    1073
Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn
                315                 320                 325

ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc    1121
Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile
            330                 335                 340

acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg    1169
Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp
            345                 350                 355

acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc    1217
Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly
360                 365                 370                 375

gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag    1265
Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln
                380                 385                 390

gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc    1313
Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg
                395                 400                 405

gtc ggg aag gtg gtg aaa gtg ttt gga gac ggg aac ctg cgt gta gca    1361
Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala
            410                 415                 420

gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac    1409
Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr
    425                 430                 435

cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag    1457
Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu
440                 445                 450                 455

aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag    1505
Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys
                460                 465                 470

agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt    1553
Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly
                475                 480                 485

aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg    1601
Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val
            490                 495                 500

gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg    1649
```

309

```
          Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu
              505             510             515

ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg        1697
Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val
520             525             530             535

gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg        1745
Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu
                540             545             550

ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg        1793
Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg
                555             560             565

gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg        1841
Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val
            570             575             580

cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt        1889
Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys
        585             590             595

gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc        1937
Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala
600             605             610             615

atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag        1985
Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu
                620             625             630

gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg        2033
Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu
                635             640             645

ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att        2081
Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile
            650             655             660

ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc        2129
Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe
665             670             675

acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag        2177
Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln
680             685             690             695

atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag        2225
Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys
                700             705             710

ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg        2273
Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu
                715             720             725

gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag        2321
Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu
```

310

```
gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg    2369
Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu
    745             750             755

ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg    2417
Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu
760             765             770             775

ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg    2465
Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr
            780             785             790

gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg    2513
Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val
            795             800             805

agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag    2561
Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu
        810             815             820

ggt cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag    2609
Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu
    825             830             835

cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg    2657
Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly
840             845             850             855

acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc    2705
Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro
            860             865             870

gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg    2753
Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu
            875             880             885

ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg    2801
Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg
        890             895             900

atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc    2849
Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg
    905             910             915

cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg    2897
Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro
920             925             930             935

cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa    2945
Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu
            940             945             950

cgc atc acc tgc ccc atc tgc atc gac agg cac atc cgc ctc gtg ttc    2993
Arg Ile Thr Cys Pro Ile Cys Ile Asp Arg His Ile Arg Leu Val Phe
            955             960             965
```

311

```
cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc   3041
Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala
         970                 975                 980

tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg   3089
Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val
     985                 990                 995

tgagccgcgc cgtccgccgc gcccgagctg ccttcgcgtg cccccgccct gtgttttata 3149

aaaagaaaga ttctcggat                                              3168


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Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr
             20                  25                  30

Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp
         35                  40                  45

Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp
     50                  55                  60

Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val
 65                  70                  75                  80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val
             85                  90                  95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr
            100                 105                 110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val
        115                 120                 125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg
    130                 135                 140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr
145                 150                 155                 160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg
                165                 170                 175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly
            180                 185                 190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val
```

```
Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys
    210             215             220

Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg
225             230             235             240

Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg
                245             250             255

Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala
            260             265             270

Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala
        275             280             285

Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly
    290             295             300

Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln
305             310             315             320

Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln
            325             330             335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln
            340             345             350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys
    355             360             365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu
    370             375             380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp
385             390             395             400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly
            405             410             415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser
            420             425             430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp
            435             440             445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu
            450             455             460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu
465             470             475             480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu
            485             490             495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala
```

```
Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu
        515                 520                 525

Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr
        530                 535                 540

Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val
545                 550                 555                 560

Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser
                565                 570                 575

Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg
        580                 585                 590

Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser
        595                 600                 605

Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly
    610                 615                 620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr
625                 630                 635                 640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His
                645                 650                 655

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp
        660                 665                 670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn
        675                 680                 685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp
    690                 695                 700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val
705                 710                 715                 720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys
                725                 730                 735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala
                740                 745                 750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly
        755                 760                 765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu
    770                 775                 780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu
785                 790                 795                 800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser
```

```
Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly
        820             825             830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro
        835             840             845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His
    850             855             860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser
865             870             875             880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val
                885             890             895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val
        900             905             910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala
        915             920             925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser
    930             935             940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp
945             950             955             960

Arg His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro
                965             970             975

Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg
        980             985             990

Asp Arg Ile Gln Ile Phe Val
        995
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<210> 161
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cactggcgcg atgcgggccg tcctctcggc tg atg ggt tgg aag ccc agc gag      113
                                    Met Gly Trp Lys Pro Ser Glu
                                    1               5

gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg     161
Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg
```

```
agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga    209
Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg
     25              30              35

gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg    257
Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val
 40              45              50                      55

ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac    305
Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp
             60              65              70

ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc    353
Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly
             75              80              85

agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc    401
Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly
         90              95              100

acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg    449
Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu
     105             110             115

ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt    497
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys
120             125             130             135

gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt    545
Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg
             140             145             150

gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag    593
Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys
             155             160             165

cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc    641
His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg
         170             175             180

cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg    689
Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg
     185             190             195

ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg    737
Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp
200             205             210             215

ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc    785
Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile
             220             225             230

cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg    833
Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp
             235             240             245
```

316

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gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg    881
Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val
        250                 255                 260

gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac    929
Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp
        265                 270                 275

cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt    977
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser
280                 285                 290                 295

gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg   1025
Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu
                300                 305  |              310

gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac   1073
Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn
                315                 320                 325

ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc   1121
Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile
                330                 335                 340

acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg   1169
Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp
        345                 350                 355

acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc   1217
Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly
360                 365                 370                 375

gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag   1265
Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln
                380                 385                 390

gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc   1313
Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg
                395                 400                 405

gtc ggg aag gtg gtg aaa gtg ttt gga gac ggg aac ctg cgt gta gca   1361
Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala
        410                 415                 420

gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac   1409
Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr
        425                 430                 435

cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag   1457
Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu
440                 445                 450                 455

aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag   1505
Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys
                460                 465                 470
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agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt   -1553-
Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly
        475   480   485

aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg   1601
Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val
        490   495   500

gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg   1649
Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu
        505   510   515

ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg   1697
Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val
520   525   530   535

gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg   1745
Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu
                540   545   550

ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg   1793
Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg
                555   560   565

gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg   1841
Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val
        570   575   580

cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt   1889
Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys
585   590   595

gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc   1937
Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala
600   605   610   615

atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag   1985
Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu
                620   625   630

gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg   2033
Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu
                635   640   645

ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att   2081
Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile
        650   655   660

ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc   2129
Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe
        665   670   675

acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag   2177
Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln
680   685   690   695

atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag   2225

318

```
     Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys
                 700             705                 710

ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg   2273
Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu
             715                 720                 725

gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag   2321
Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu
             730                 735                 740

gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg   2369
Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu
             745                 750                 755

ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg   2417
Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu
760                 765                 770                 775

ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg   2465
Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr
             780                 785                 790

gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg   2513
Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val
             795                 800                 805

agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag   2561
Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu
             810                 815                 820

ggt cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag   2609
Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu
             825                 830                 835

cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg   2657
Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly
840                 845                 850                 855

acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc   2705
Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro
             860                 865                 870

gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg   2753
Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu
             875                 880                 885

ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg   2801
Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg
             890                 895                 900

atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc   2849
Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg
905                 910                 915

cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg   2897
Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro
```

319

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cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa   2945
Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu
                940                     945                 950

cgc atc acc tgc ccc atc tgc atc gac agc cac atc cgc ctc gtg ttc   2993
Arg Ile Thr Cys Pro Ile Cys Ile Asp Ser His Ile Arg Leu Val Phe
                955                     960                 965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc   3041
Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala
                970                     975                 980

tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg   3089
Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val
            985                     990                 995

tgagccgcgc cgtccgccgc gcccgagctg ccttcgcgtg cccccgccct gtgttttata   3149

aaaagaaaga ttctcggat                                                 3168
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<210> 162
<211> 999
<212> PRT
<213> Homo sapiens

<400> 162

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Met Gly Trp Lys Pro Ser Glu Ala Arg Gly Gln Ser Gln Ser Leu Gln
 1               5                  10                  15

Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr
            20                  25                  30

Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp
            35                  40                  45

Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp
        50                  55                  60

Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val
65                  70                  75                  80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val
                85                  90                  95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr
            100                 105                 110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val
        115                 120                 125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg
        130                 135                 140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr
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Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg
           165   170   175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly
           180   185   190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val
           195   200   205

Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys
   210   215   220

Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg
225   230   235   240

Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg
           245   250   255

Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala
           260   265   270

Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala
           275   280   285

Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly
           290   295   300

Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln
305   310   315   320

Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln
           325   330   335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln
           340   345   350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys
           355   360   365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu
           370   375   380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp
385   390   395   400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly
           405   410   415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser
           420   425   430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp
           435   440   445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu

321

```
Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu
465             470             475             480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu
                485             490             495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala
            500             505             510

Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu
            515             520             525

Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr
            530             535             540

Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val
545             550             555             560

Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser
                565             570             575

Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg
                580             585             590

Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser
                595             600             605

Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly
            610             615             620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr
625             630             635             640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His
                645             650             655

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp
                660             665             670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn
            675             680             685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp
            690             695             700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val
705             710             715             720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys
                725             730             735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala
            740             745             750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly
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322

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu
    770   775   780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu
785   790   795   800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser
                805   810   815

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly
                820   825   830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro
            835   840   845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His
    850   855   860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser
865   870   875   880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val
                885   890   895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val
            900   905   910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala
            915   920   925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser
    930   935   940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp
945   950   955   960

Ser His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro
                965   970   975

Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg
            980   985   990

Asp Arg Ile Gln Ile Phe Val
        995

<210> 163
<211> 4031
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (91)..(2649)

323

<400>_163

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tcccgtcgcc aatccccgcc gtcccgggcc atg atc gcc tgg cgt ctg ccc ttg   114
                                  Met Ile Ala Trp Arg Leu Pro Leu
                                   1               5

tgc gtg ctc ttg gtg gcc tcc gtc gag agc cac ctg ggg gcc ctg ggg   162
Cys Val Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Ala Leu Gly
     10                  15                  20

ccc aag aac gtc tcg cag aaa gac gcg gag ttt gag cgc acc tac gcg   210
Pro Lys Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Ala
 25                  30                  35                  40

gac gac gtc aac agc gag ctg gtc aac atc tac acc ttc aac cac acc   258
Asp Asp Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr
                 45                  50                  55

gtg acc cgc aac cgg acc gag ggt gtg cga gtg tct gtg aat gtc ctg   306
Val Thr Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu
                 60                  65                  70

aac aag cag aaa ggg gcg cct ttg ctg ttc gtg gtc cgc cag aag gag   354
Asn Lys Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu
             75                  80                  85

gct gtt gtg tcc ttc cag gtg ccc cta atc ctt cga gga ctg tat cag   402
Ala Val Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Leu Tyr Gln
         90                  95                  100

cgg aag tac ctc tac caa aaa gtg gaa cga act ctg tgt cag ccc ccc   450
Arg Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
105                 110                 115                 120

acc aag aat gag tct gag atc cag ttt ttc tat gtg gac gtg tct acc   498
Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr
                125                 130                 135

ctg tca ccc gtc aat acc act tac cag ctc cga gtc aac cgt gtg gac   546
Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Asn Arg Val Asp
                140                 145                 150

aat ttt gtg ctc agg act gga gag ctg ttt acc ttt aat acc act gca   594
Asn Phe Val Leu Arg Thr Gly Glu Leu Phe Thr Phe Asn Thr Thr Ala
             155                 160                 165

gcc cag ccc cag tac ttc aaa tac gag ttt cct gat ggt gtg gac tcg   642
Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Asp Gly Val Asp Ser
         170                 175                 180

gta att gtc aag gtg acc tcc aag aag gcc ttc ccc tgc tca gtc atc   690
Val Ile Val Lys Val Thr Ser Lys Lys Ala Phe Pro Cys Ser Val Ile
185                 190                 195                 200

tcc atc cag gat gtc ctg tgc cct gtc tat gat ctg gac aac agt gta   738
Ser Ile Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Ser Val
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324

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gcc ttc att ggc atg tac cag acg atg act aag aag gca gcc atc act    786
Ala Phe Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr
        220             225             230

gtg cag cgg aaa gac ttc ccc agc aac agc ttc tat gtg gtg gtg gta    834
Val Gln Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val
        235             240             245

gtg aag act gag gac cag gcc tgc gga ggg tcc ttg ccc ttc tac cct    882
Val Lys Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro
        250             255             260

ttt gtg gaa gat gag cca gtg gat caa ggg cac cgt cag aaa aca ctg    930
Phe Val Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu
265             270             275             280

tca gtg ctg gtc tct cag gct gtc aca tct gag gcc tat gtt ggt ggg    978
Ser Val Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Gly Gly
            285             290             295

atg ctc ttt tgc ctg ggc ata ttc ttg tcc ttc tac ctg ctg act gtg   1026
Met Leu Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val
        300             305             310

ctg ctg gcc tgt tgg gag aac tgg agg caa agg aag aag acc ttg ctg   1074
Leu Leu Ala Cys Trp Glu Asn Trp Arg Gln Arg Lys Lys Thr Leu Leu
        315             320             325

gtg gcc ata gac cga gcc tgc cca gaa agt ggt cac gct cgg gtc ttg   1122
Val Ala Ile Asp Arg Ala Cys Pro Glu Ser Gly His Ala Arg Val Leu
        330             335             340

gct gat tca ttt cct ggc agt gcc cct tac gag ggt tac aac tat ggc   1170
Ala Asp Ser Phe Pro Gly Ser Ala Pro Tyr Glu Gly Tyr Asn Tyr Gly
345             350             355             360

tcc ttt gaa aat ggt tcc gga tcc act gac ggg ttg gtt gaa agc gca   1218
Ser Phe Glu Asn Gly Ser Gly Ser Thr Asp Gly Leu Val Glu Ser Ala
            365             370             375

ggt tca ggg gac ctc tcc tac agt tac cag ggg cac gac cag ttc aag   1266
Gly Ser Gly Asp Leu Ser Tyr Ser Tyr Gln Gly His Asp Gln Phe Lys
        380             385             390

cgg cgc ctt ccc tct ggc cag atg cgg cag ctg tgc att gcc atg gac   1314
Arg Arg Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Asp
        395             400             405

cgc tcc ttt gac gca gtg ggt cct cgg cct cga ctg gac tcc atg agc   1362
Arg Ser Phe Asp Ala Val Gly Pro Arg Pro Arg Leu Asp Ser Met Ser
        410             415             420

tcc gtg gaa gag gat gac tac gac acg ctg act gac atc gac tca gac   1410
Ser Val Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp
425             430             435             440
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325

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aaa aac gtc att cga acc aag caa tac ctc tgt gtg gct gat ctg gca    1458
Lys Asn Val Ile Arg Thr Lys Gln Tyr Leu Cys Val Ala Asp Leu Ala
                445               450               455

cga aag gac aaa cgt gtt ttg cgg aaa aag tac cag att tac ttc tgg    1506
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp
                460               465               470

aac ata gcc acc att gcg gtc ttc tac gca ctt cct gtg gtg cag ctg    1554
Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu
                475               480               485

gtg atc acc tac cag acg gtg gtg aat gtc aca ggg aac cag gac atc    1602
Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile
                490               495               500

tgc tac tac aac ttc ctc tgt gcc cac ccg ctg ggc aac ctc agc gcc    1650
Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala
505               510               515               520

ttc aac aac atc ctc agc aac ttg ggg tac atc ctg ctg ggg ctg ctc    1698
Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu
                525               530               535

ttc ctg ctc atc atc ctg cag cga gag atc aat cat aac cgg gcc ctg    1746
Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu
                540               545               550

ctg cgg aat gac ctc tat gct ctg gag tgt ggg atc ccc aaa cac ttt    1794
Leu Arg Asn Asp Leu Tyr Ala Leu Glu Cys Gly Ile Pro Lys His Phe
                555               560               565

ggt ctg ttt tac gcc atg ggc aca gca ctg atg atg gag ggg cta ctt    1842
Gly Leu Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu
                570               575               580

agt gcc tgt tac cac gtc tgc ccc aac tac acc aac ttc cag ttt gat    1890
Ser Ala Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp
585               590               595               600

acc tcc ttc atg tac atg att gct ggc ctc tgc atg ctg aag ctc tac    1938
Thr Ser Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr
                605               610               615

cag aag cgg cac cca gat atc aac gcc agt gcc tac agt gca tat gcc    1986
Gln Lys Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala
                620               625               630

tgc ttg gcc atc gtc atc ttc ttc tcc gtt ctg ggc gtg gtg ttt ggc    2034
Cys Leu Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly
                635               640               645

aaa ggg aac acg gcc ttc tgg att gtc ttc tcc gtc att cac atc atc    2082
Lys Gly Asn Thr Ala Phe Trp Ile Val Phe Ser Val Ile His Ile Ile
                650               655               660
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326

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tcc acc ctg ctc ctc agc act cag ctc tat tac atg ggc cgc tgg aag    2130
Ser Thr Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys
665             670             675             680

ctg gac ttc ggg atc ttc cgc cgc atc ctc cat gtg ctc tac aca gac    2178
Leu Asp Phe Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp
                685             690             695

tgc atc cgg cag tgc agc ggg ccc ctt tac acg gac cgc atg gtg ctt    2226
Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Thr Asp Arg Met Val Leu
            700             705             710

ctg gtc atg ggc aac att atc aac tgg tcg ctg gct gca tac gga ctc    2274
Leu Val Met Gly Asn Ile Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu
            715             720             725

atc atg cgc ccc aat gac ttt gct tcc tac ttg ctg gca att ggc atc    2322
Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile
        730             735             740

tgc aac ctg ctg ctt tat ttc gcc ttc tac atc atc atg aag ctc cgg    2370
Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg
745             750             755             760

agc ggc gag agg atc aag ctc atc cct ctg ctt tgc atc gtc tgc acc    2418
Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr
                765             770             775

tcc gtg gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctg agc    2466
Ser Val Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser
            780             785             790

acg tgg cag aaa acc ccc gca gag tcc agg gag cac aac cgc gac tgc    2514
Thr Trp Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys
        795             800             805

atc ctc ctc gac ttc ttt gat gac cac gat atc tgg cac ttc ctg tcc    2562
Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser
    810             815             820

tcc att gcc atg ttt ggg tcc ttc ctg gtt ttg ctg acg ttg gat gac    2610
Ser Ile Ala Met Phe Gly Ser Phe Leu Val Leu Leu Thr Leu Asp Asp
825             830             835             840

gac ttg gac aca gta cag cgg gac aag atc tat gtc ttc tagcagcatc    2659
Asp Leu Asp Thr Val Gln Arg Asp Lys Ile Tyr Val Phe
            845             850

tgtggtccag gcttcacctc acgggcctag cgcctgcctc tgcatcacct gccagttgcc    2719

acaagaacac cacgggtgtg agtcccagct ctgctgccca gcattggatg tcgtggcaag    2779

acagcgagat tccagcccag gcctgactca ggacagttcc tggtggcact gagccttgga    2839

gttgcctctg cggaggagga ggcctgctcc gcattcccca gacactggcc aaattgctgc    2899

tttcttctca gtgttgggtc ctccccagga ccctagtctg tccatctgtc ttgtttatcc    2959
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327

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actggctctc catttgtccc tttggagagg aaggtgggaa ggcaatgtcc tgtcccattt 3019

catgccttgc attctgccca tcccttccct cctctcagct taggacacac agccctttct 3079

tcttcccatg ctctgtccag gaccacagtc tggtgcctga ttctttgtcc atcaccagga 3139

cctaagctct ccctgggtct gtagctggct gctatcactg cccactctga cctgccagga 3199

cagatgcagg taggagactt tgggggctgg ccagctggtg ccaggctttc ggtgctaagg 3259

cctggaaggg gcctaggtac gaccctcctc cctgacctgt gcttggagct ggctcttcag 3319

cagtgagggc cagcccaagt tgagtcttct gatcgggggac tgaattcaga ggccacctca 3379

tcccaccagc cactagaatg atgccagcac tagggttggt gggaagtggc aactcactgt 3439

ccccttccac accctcagtc ctgccaagcc ccagatgggg gcctctcagt gccattgaca 3499

ctgcccaaga atgtctagag gccacggaac ggtgccaagc acacagtccc ttttgcctct 3559

ttcacgggag caggagtccc agtgcctgtc gtggaaaggg aggaacatgc caggtccctg 3619

tgtgtccttg gccctgtctc accaaaggac tcagggctgg tttctgagtt ccgtccagt 3679

atttagccaa gttctgtgtt agtcacgtag gcctaagagc cttggcgttt acagagtcac 3739

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agtgggcccc aggaatgtgt ttccttctct ccaccatgtt tttatagctc ttgggctggg 3919

agaagaggcg ggtctgggtc tttgtttctg agctttgttc tatgttcctc catgctacgg 3979

ttgcaattgt tttctatgaa cgagtacatt caataaagac aaccagacct gg          4031
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<212> PRT
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<400> 164

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Glu Ser His Leu Gly Ala Leu Gly Pro Lys Asn Val Ser Gln Lys Asp
            20                  25                  30

Ala Glu Phe Glu Arg Thr Tyr Ala Asp Asp Val Asn Ser Glu Leu Val
        35                  40                  45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
    50                  55                  60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu
```

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro
                85   90   95

Leu Ile Leu Arg Gly Leu Tyr Gln Arg Lys Tyr Leu Tyr Gln Lys Val
                100   105   110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
            115   120   125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
    130   135   140

Gln Leu Arg Val Asn Arg Val Asp Asn Phe Val Leu Arg Thr Gly Glu
145   150   155   160

Leu Phe Thr Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
                165   170   175

Glu Phe Pro Asp Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Lys
            180   185   190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
            195   200   205

Val Tyr Asp Leu Asp Asn Ser Val Ala Phe Ile Gly Met Tyr Gln Thr
    210   215   220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
225   230   235   240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
                245   250   255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Val Glu Asp Glu Pro Val Asp
                260   265   270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
            275   280   285

Thr Ser Glu Ala Tyr Val Gly Gly Met Leu Phe Cys Leu Gly Ile Phe
    290   295   300

Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
305   310   315   320

Arg Gln Arg Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
                325   330   335

Glu Ser Gly His Ala Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ala
            340   345   350

Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Gly Ser Gly Ser
    355   360   365

Thr Asp Gly Leu Val Glu Ser Ala Gly Ser Gly Asp Leu Ser Tyr Ser

329

Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met
385   390   395   400

Arg Gln Leu Cys Ile Ala Met Asp Arg Ser Phe Asp Ala Val Gly Pro
            405   410   415

Arg Pro Arg Leu Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp
            420   425   430

Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln
            435   440   445

Tyr Leu Cys Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg
            450   455   460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe
465   470   475   480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val
            485   490   495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala
            500   505   510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu
            515   520   525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg
            530   535   540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Tyr Ala Leu
545   550   555   560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
            565   570   575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro
            580   585   590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala
            595   600   605

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn
            610   615   620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe
625   630   635   640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile
            645   650   655

Val Phe Ser Val Ile His Ile Ile Ser Thr Leu Leu Leu Ser Thr Gln
            660   665   670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Phe Gly Ile Phe Arg Arg

330

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
    690   695   700

Leu Tyr Thr Asp Arg Met Val Leu Leu Val Met Gly Asn Ile Ile Asn
705   710   715   720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
                725   730   735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
                740   745   750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
        755   760   765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
    770   775   780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
785   790   795   800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
                805   810   815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
                820   825   830

Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln Arg Asp
        835   840   845

Lys Ile Tyr Val Phe
    850

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<211> 3138
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (84)..(2648)

<400> 165
gccgcaaccc gtcccggagg tgtcctgtct cctgtcgccg ccgccgccgc caccaccgct 60

gccactgccg ccctgccggg gcc atg ttc gct ctg ggc ttg ccc ttc ttg gtg 113
                          Met Phe Ala Leu Gly Leu Pro Phe Leu Val
                           1   5   10

ctc ttg gtg gcc tcg gtc gag agc cat ctg ggg gtt ctg ggg ccc aag   161
Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Val Leu Gly Pro Lys
            15   20   25

aac gtc tcg cag aaa gac gcc gag ttt gag cgc acc tac gtg gac gag   209

331

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      Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu      —
                  30                  35                  40

gtc aac agc gag ctg gtc aac atc tac acc ttc aac cat act gtg acc      257
Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr
            45                  50                  55

cgc aac agg aca gag ggc gtg cgt gtg tct gtg aac gtc ctg aac aag      305
Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys
        60                  65                  70

cag aag ggg gcg ccg ttg ctg ttt gtg gtc cgc cag aag gag gct gtg      353
Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
75                  80                  85                  90

gtg tcc ttc cag gtg ccc cta atc ctg cga ggg atg ttt cag cgc aag      401
Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg Lys
                95                  100                 105

tac ctc tac caa aaa gtg gaa cga acc ctg tgt cag ccc ccc acc aag      449
Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys
                110                 115                 120

aat gag tcg gag att cag ttc ttc tac gtg gat gtg tcc acc ctg tca      497
Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr Leu Ser
                125                 130                 135

cca gtc aac acc aca tac cag ctc cgg gtc agc cgc atg gac gat ttt      545
Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg Met Asp Asp Phe
        140                 145                 150

gtg ctc agg act ggg gag cag ttc agc ttc aat acc aca gca gca cag      593
Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln
155                 160                 165                 170

ccc cag tac ttc aag tat gag ttc cct gaa ggc gtg gac tcg gta att      641
Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu Gly Val Asp Ser Val Ile
                175                 180                 185

gtc aag gtg acc tcc aac aag gcc ttc ccc tgc tca gtc atc tcc att      689
Val Lys Val Thr Ser Asn Lys Ala Phe Pro Cys Ser Val Ile Ser Ile
                190                 195                 200

cag gat gtg ctg tgt cct gtc tat gac ctg gac aac aac gta gcc ttc      737
Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Asn Val Ala Phe
        205                 210                 215

atc ggc atg tac cag acg atg acc aag aag gcg gcc atc acc gta cag      785
Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr Val Gln
        220                 225                 230

cgc aaa gac ttc ccc agc aac agc ttt tat gtg gtg gtg gtg gtg aag      833
Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val Val Lys
235                 240                 245                 250

acc gaa gac caa gcc tgc ggg ggc tcc ctg cct ttc tac ccc ttc gca      881
Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala
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332

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gaa gat gaa ccg gtc gat caa ggg cac cgc cag aaa acc ctg tca gtg      929
Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val
            270             275             280

ctg gtg tct caa gca gtc acg tct gag gca tac gtc agt ggg atg ctc      977
Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu
        285             290             295

ttt tgc ctg ggt ata ttt ctc tcc ttt tac ctg ctg acc gtc ctc ctg      1025
Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu
        300             305             310

gcc tgc tgg gag aac tgg agg cag aag aag aag acc ctg ctg gtg gcc      1073
Ala Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala
315             320             325             330

att gac cga gcc tgc cca gaa agc ggt cac cct cga gtc ctg gct gat      1121
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala Asp
            335             340             345

tct ttt cct ggc agt tcc cct tat gag ggt tac aac tat ggc tcc ttt      1169
Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe
            350             355             360

gag aat gtt tct gga tct acc gat ggt ctg gtt gac agc gct ggc act      1217
Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser Ala Gly Thr
        365             370             375

ggg gac ctc tct tac ggt tac cag ggg cac gac cag ttc aag cgg cgc      1265
Gly Asp Leu Ser Tyr Gly Tyr Gln Gly His Asp Gln Phe Lys Arg Arg
    380             385             390

ctc ccc tct ggc cag atg cgg cag ctg tgc att gcc atg ggc cgc tcc      1313
Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Gly Arg Ser
395             400             405             410

ttt gaa cct gta ggt act cgg ccc cga gtg gac tcc atg agc tct gtg      1361
Phe Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val
            415             420             425

gag gag gat gac tac gac aca ttg acc gac atc gat tcc gac aag aat      1409
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn
            430             435             440

gtc att cgc acc aag caa tac ctc tat gtg gct gac ctg gca cgg aag      1457
Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys
        445             450             455

gac aag cgt gtt ctg cgg aaa aag tac cag atc tac ttc tgg aac att      1505
Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile
    460             465             470

gcc acc att gct gtc ttc tat gcc ctt cct gtg gtg cag ctg gtg atc      1553
Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val Ile
475             480             485             490
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333

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acc tac cag acg gtg gtg aat gtc aca ggg aat cag gac atc tgc tac    1601
Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr
            495             500               505

tac aac ttc ctc tgc gcc cac cca ctg ggc aat ctc agc gcc ttc aac    1649
Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn
            510             515               520

aac atc ctc agc aac ctg ggg tac atc ctg ctg ggg ctg ctt ttc ctg    1697
Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu
            525             530               535

ctc atc atc ctg caa cgg gag atc aac cac aac cgg gcc ctg ctg cgc    1745
Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg
        540             545               550

aat gac ctc tgt gcc ctg gaa tgt ggg atc ccc aaa cac ttt ggg ctt    1793
Asn Asp Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe Gly Leu
555             560             565               570

ttc tac gcc atg ggc aca gcc ctg atg atg gag ggg ctg ctc agt gct    1841
Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu Ser Ala
            575             580               585

tgc tat cat gtg tgc ccc aac tat acc aat ttc cag ttt gac aca tcg    1889
Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser
            590             595               600

ttc atg tac atg atc gcc gga ctc tgc atg ctg aag ctc tac cag aag    1937
Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys
            605             610               615

cgg cac ccg gac atc aac gcc agc gcc tac agt gcc tac gcc tgc ctg    1985
Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu
        620             625               630

gcc att gtc atc ttc ttc tct gtg ctg ggc gtg gtc ttt ggc aaa ggg    2033
Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly
635             640             645               650

aac acg gcg ttc tgg atc gtc ttc tcc atc att cac atc atc gcc acc    2081
Asn Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr
            655             660               665

ctg ctc ctc agc acg cag ctc tat tac atg ggc cgg tgg aaa ctg gac    2129
Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp
            670             675               680

tcg ggg atc ttc cgc cgc atc ctc cac gtg ctc tac aca gac tgc atc    2177
Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile
            685             690               695

cgg cag tgc agc ggg ccg ctc tac gtg gac cgc atg gtg ctg ctg gtc    2225
Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val
        700             705               710
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334

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atg ggc aac gtc atc aac tgg tcg ctg gct gcc tat ggg ctt atc atg    2273
Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met
715             720             725             730

cgc ccc aat gat ttc gct tcc tac ttg ttg gcc att ggc atc tgc aac    2321
Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn
            735             740             745

ctg ctc ctt tac ttc gcc ttc tac atc atc atg aag ctc cgg agt ggg    2369
Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly
            750             755             760

gag agg atc aag ctc atc ccc ctg ctc tgc atc gtt tgc acc tcc gtg    2417
Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val
        765             770             775

gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctc agc acc tgg    2465
Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp
        780             785             790

cag aaa acc cct gca gag tcg agg gag cac aac cgg gac tgc atc ctc    2513
Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys Ile Leu
795             800             805             810

ctc gac ttc ttt gac gac cac gac atc tgg cac ttc ctc tcc tcc atc    2561
Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser Ser Ile
            815             820             825

gcc atg ttc ggg tcc ttc ctg gta agc ggg cct ccc ggc cga gcc ggg    2609
Ala Met Phe Gly Ser Phe Leu Val Ser Gly Pro Pro Gly Arg Ala Gly
            830             835             840

tgg gta cgt gaa ggt agc agc tgc ctc ctt ccc tgt ggc tgatctggcg    2658
Trp Val Arg Glu Gly Ser Ser Cys Leu Leu Pro Cys Gly
        845             850             855

tccacacccc aggtgttgct gacactggat gacgacctgg atacttagaa aggggcttca  2718

ggaagggatg tgctgtttcc ctctacgtgc ccagtcctag cctcgctcta ggacccaggg  2778

ctggcttcta agtttccgtc cagtcttcag gcaagttctg tgttagtcat gcacacacat  2838

acctatgaaa ccttggagtt tacaaagaat tgccccagct ctgggcaccc tggccaccct  2898

ggtccttgga tccccttcgt cccacctggt ccaccccaga tgctgaggat gggggagctc  2958

aggcggggcc tctgctttgg ggatgggaat gtgttttct cccaaacttg tttttatagc   3018

tctgcttgaa gggctgggag atgaggtggg tctggatctt ttctcagagc gtctccatgc  3078

tatggttgca tttccgtttt ctatgaatga atttgcattc aataaacaac cagactcagt  3138


<210> 166
<211> 855
<212> PRT
<213> Homo sapiens
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335

<400> 166

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Met Phe Ala Leu Gly Leu Pro Phe Leu Val Leu Leu Val Ala Ser Val
 1               5                  10                  15

Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln Lys Asp
            20                  25                  30

Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser Glu Leu Val
            35                  40                  45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
        50                  55                  60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu
65                  70          ·        75                  80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro
                85                  90                  95

Leu Ile Leu Arg Gly Met Phe Gln Arg Lys Tyr Leu Tyr Gln Lys Val
            100                 105                 110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
        115                 120                 125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
        130                 135                 140

Gln Leu Arg Val Ser Arg Met Asp Asp Phe Val Leu Arg Thr Gly Glu
145                 150                 155                 160

Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
            165                 170                 175

Glu Phe Pro Glu Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn
            180                 185                 190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
            195                 200                 205

Val Tyr Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr
        210                 215                 220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
225                 230                 235                 240

Asn Ser Phe Tyr Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
            245                 250                 255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro Val Asp
            260                 265                 270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
        275                 280                 285

Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys Leu Gly Ile Phe
```

336

Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
305   310   315   320

Arg Gln Lys Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
                325   330   335

Glu Ser Gly His Pro Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ser
                340   345   350

Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Val Ser Gly Ser
                355   360   365

Thr Asp Gly Leu Val Asp Ser Ala Gly Thr Gly Asp Leu Ser Tyr Gly
                370   375   380

Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met   ?
385   390   395   400

Arg Gln Leu Cys Ile Ala Met Gly Arg Ser Phe Glu Pro Val Gly Thr
                405   410   415

Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp
                420   425   430

Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln
                435   440   445

Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg
                450   455   460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe
465   470   475   480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val
                485   490   495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala
                500   505   510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu
                515   520   525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg
                530   535   540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu
545   550   555   560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
                565   570   575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro
                580   585   590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala

337

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn
    610   615   620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe
625   630   635   640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile
            645   650   655

Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu Leu Ser Thr Gln
        660   665   670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly Ile Phe Arg Arg
        675   680   685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
    690   695   700

Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly Asn Val Ile Asn
705   710   715   720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
            725   730   735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
        740   745   750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
        755   760   765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
    770   775   780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
785   790   795   800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
            805   810   815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
        820   825   830

Leu Val Ser Gly Pro Pro Gly Arg Ala Gly Trp Val Arg Glu Gly Ser
        835   840   845

Ser Cys Leu Leu Pro Cys Gly
    850   855

<210> 167
<211> 2815
<212> DNA
<213> Homo sapiens

<220>

338

<221> -CDS
<222> (56)..(571)

<400> 167
gcgaagcgcg cctgcgaccc ggcgtccggg cgcgctggag aggacgcgag gagcc atg 58
                                                                Met
                                                                1

agg cgc cag cct gcg aag gtg gcg gcg ctg ctg ctc ggg ctg ctc ttg 106
Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu Leu
              5   10   15

gag tgc aca gaa gcc aaa aag cat tgc tgg tat ttc gaa gga ctc tat 154
Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu Tyr
         20   25   30

cca acc tat tat ata tgc cgc tcc tac gag gac tgc tgt ggc tcc agg 202
Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg
     35   40   45

tgc tgt gtg cgg gcc ctc tcc ata cag agg ctg tgg tac ttc tgg ttc 250
Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp Phe
50   55   60   65

ctt ctg atg atg ggc gtg ctt ttc tgc tgc gga gcc ggc ttc ttc atc 298
Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile
                70   75   80

cgg agg cgc atg tac ccc ccg ccg ctg atc gag gag cca gcc ttc aat 346
Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn
                85   90   95

gtg tcc tac acc agg cag ccc cca aat ccc ggc cca gga gcc cag cag 394
Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln
         100   105   110

ccg ggg ccg ccc tat tac acc gac cca gga gga ccg ggg atg aac cct 442
Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro
  .115   120   125

gtc ggg aat tcc atg gca atg gct ttc cag gtc cca ccc aac tca ccc 490
Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro
130   135   140   145

cag ggg agt gtg gcc tgc ccg ccc cct cca gcc tac tgc aac acg cct 538
Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro
                150   155   160

ccg ccc ccg tac gaa cag gta gtg aag gcc aag tagtggggtg cccacgtgca 591
Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys
                165   170

agaggaggga caggagaggg cctttccctg gcctttctgt cttcgttgat gttcacttcc 651

aggaacggtc tcgtgggctg ctaagggcag ttcctctgat atcctcacag caagcacagc 711

tctctttcag gctttccatg gagtacaata tatgaactca cactttgtct cctctgttgc 771

339

ttctgtttct gacgcagtct gtgctctcac atggtagtgt ggtgacagtc cccgagggct 831

gacgtcctta cggtggcgtg accagatcta cgggagagag actgagagga agaaggcagt 891

gctggaggtg caggtggcat gtagaggggc caggccgagc atcccaggca agcatccttc 951

tgcccgggta ttaataggaa gccccatgcc gggcggctca gccgatgaag cagcagccga 1011

ctgagctgag cccagcaggt catctgctcc agcctgtcct ctcgtcagcc ttcctcttcc 1071

agaagctgtt ggagagacat tcaggagaga gcaagcccct tgtcatgttt ctgtctctgt 1131

tcatatccta aagatagact tctcctgcac cgccagggaa gggtagcacg tgcagctctc 1191

accgcaggat ggggcctaga atcaggcttg ccttggaggc ctgacagtga tctgacatcc 1251

actaagcaaa tttatttaaa ttcatgggaa atcacttcct gccccaaact gagacattgc 1311

attttgtgag ctcttggtct gatttggaga aaggactgtt acccattttt ttggtgtgtt 1371

tatggaagtg catgtagagc gtcctgccct ttgaaatcag actgggtgtg tgtcttccct 1431

ggacatcact gcctctccag ggcattctca ggcccggggg tctccttccc tcaggcagct 1491

ccagtggtgg gttctgaagg gtgctttcaa aacggggcac atctggctgg gaagtcacat 1551

ggactcttcc agggagagag accagctgag gcgtctctct ctgaggttgt gttgggtcta 1611

agcgggtgtg tgctgggctc caaggaggag gagcttgctg gggaaagaca ggagaagtac 1671

tgactcaact gcactgacca tgttgtcata attagaataa agaagaagtg gtcggaaatg 1731

cacattcctg gataggaatc acagctcacc ccaggatctc acaggtagtc tcctgagtag 1791

ttgacggcta gcggggagct agttccgccg catagttata gtgttgatgt gtgaacgctg 1851

acctgtcctg tgtgctaaga gctatgcagc ttagctgagg cgcctagatt actagatgtg 1911

ctgtatcacg gggaatgagg tgggggtgct tattttttaa tgaactaatc agagcctctt 1971

gagaaattgt tactcattga actggagcat caagacatct catggaagtg gatacggagt 2031

gatttggtgt ccatgctttt cactctgagg acatttaatc ggagaacctc ctggggaatt 2091

ttgtgggaga cacttgggaa caaaacagac accctgggaa tgcagttgca agcacagatg 2151

ctgccaccag tgtctctgac caccctggtg tgactgctga ctgccagcgt ggtacctccc 2211

atgctgcagg cctccatcta aatgagacaa caaagcacaa tgttcactgt ttacaaccaa 2271

gacaactgcg tgggtccaaa cactcctctt cctccaggtc atttgttttg cattttttaat 2331

gtctttattt tttgtaatga aaaagcacac taagctgccc ctggaatcgg gtgcagctga 2391

ataggcaccc aaaagtccgt gactaaattt cgtttgtctt tttgatagca aattatgtta 2451

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agagacagtg atggctaggg ctcaacaatt ttgtattccc atgtttgtgt gagacagagt 2511

ttgttttccc ttgaacttgg ttagaattgt gctactgtga acgctgatcc tgcatatgga 2571

agttccgctt cggtgacatt tcctggccat tcttgtttcc attgtgtgga tggtgggttg 2631

tgcccacttc ctggagtgag acagctcctg gtgtgtagaa ttcccggagc gtccgtggtt 2691

cagagtaaac ttgaagcaga tctgtgcatg cttttcctct gcaacaattg gctcgtttct 2751

ctttttgtt ctcttttgat aggatcctgt ttcctatgtg tgcaaaataa aaataaattt 2811

gggc                                                              2815


<210> 168
<211> 172
<212> PRT
<213> Homo sapiens

<400> 168
Met Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu
 1               5                   10                  15

Leu Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu
            20                  25                  30

Tyr Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser
        35                  40                  45

Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp
    50                  55                  60

Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe
65                  70                  75                  80

Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe
                85                  90                  95

Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln
            100                 105                 110

Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn
        115                 120                 125

Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser
    130                 135                 140

Pro Gln Gly Ser Val Ala Cys Pro Pro Pro Ala Tyr Cys Asn Thr
145                 150                 155                 160

Pro Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys
                165                 170


<210> 169
<211> 3337
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (136)..(1755)

<400> 169
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tacccgagtc tcgtttcctc tcagtccatc caccctttcat ggggccagag ccctctctcc 120

agaatctgag cagca atg ccg ttt gct gaa gac aag acc tat aag tat atc 171
               Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile
                1   5   10

tgc cgc aat ttc agc aat ttt tgc aat gtg gat gtt gta gag att ctg 219
Cys Arg Asn Phe Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu
         15   20   25

cct tac ctg ccc tgc ctc aca gca aga gac cag gat cga ctg cgg gcc 267
Pro Tyr Leu Pro Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala
     30   35   40

acc tgc aca ctc tca ggg aac cgg gac acc ctc tgg cat ctc ttc aat 315
Thr Cys Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn
 45   50   55   60

acc ctt cag cgg cgg ccc ggc tgg gtg gag tac ttc att gcg gca ctg 363
Thr Leu Gln Arg Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu
             65   70   75

agg ggc tgt gag cta gtt gat ctc gcg gac gaa gtg gcc tct gtc tac 411
Arg Gly Cys Glu Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr
             80   85   90

cag agc tac cag cct cgg acc tcg gac cgt ccc cca gac cca ctg gag 459
Gln Ser Tyr Gln Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu
         95   100   105

cca ccg tca ctt cct gct gag agg cca ggg ccc ccc aca cct gct gcg 507
Pro Pro Ser Leu Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala
     110   115   120

gcc cac agc atc ccc tac aac agc tgc aga gag aag gag cca agt tac 555
Ala His Ser Ile Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr
125   130   135   140

ccc atg cct gtc cag gag acc cag gcg cca gag tcc cca gga gag aat 603
Pro Met Pro Val Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn
             145   150   155

tca gag caa gcc ctg cag acg ctc agc ccc aga gcc atc cca agg aat 651
Ser Glu Gln Ala Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn
             160   165   170

cca gat ggt ggc ccc ctg gag tcc tcc tct gac ctg gca gcc ctc agc 699

342

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      Pro Asp Gly Gly Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser
          175                 180                 185

cct ctg acc tcc agc ggg cat cag gag cag gac aca gaa ctg ggc agt    747
Pro Leu Thr Ser Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser
    190                 195                 200

acc cac aca gca ggt gcg acc tcc agc ctc aca cca tcc cgt ggg cct    795
Thr His Thr Ala Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro
205                 210                 215                 220

gtg tct cca tct gtc tcc ttc cag ccc ctg gcc cgt tcc acc ccc agg    843
Val Ser Pro Ser Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg
                225                 230                 235

gca agc cgc ttg cct gga ccc aca ggg tca gtt gta tct act ggc acc    891
Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr
            240                 245                 250

tcc ttc tcc tcc tca tcc cct ggc ttg gcc tct gca ggg gct gca gag    939
Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu
        255                 260                 265

ggt aaa cag ggt gca gag agt gac cag gcc gag cct atc atc tgc tcc    987
Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser
    270                 275                 280

agt ggg gca gag gca cct gcc aac tct ctg ccc tcc aaa gtg cct acc    1035
Ser Gly Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr
285                 290                 295                 300

acc ttg atg cct gtg aac aca gtg gcc ctg aaa gtg cct gcc aac cca    1083
Thr Leu Met Pro Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro
                305                 310                 315

gca tct gtc agc aca gtg ccc tcc aag ttg cca act agc tca aag ccc    1131
Ala Ser Val Ser Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro
                320                 325                 330

cct ggt gca gtg cct tct aat gcg ctc acc aat cca gca cca tcc aaa    1179
Pro Gly Ala Val Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys
        335                 340                 345

ttg ccc atc aac tca acc cgt gct ggc atg gtg cca tcc aaa gtg cct    1227
Leu Pro Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro
    350                 355                 360

act agc atg gtg ctc acc aag gtg tct gcc agc aca gtc ccc act gac    1275
Thr Ser Met Val Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp
365                 370                 375                 380

ggg agc agc aga aat gag gag acc cca gca gct cca aca ccc gcc ggc    1323
Gly Ser Ser Arg Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly
                385                 390                 395

gcc act gga ggc agc tca gcc tgg cta gac agc agc tct gag aat agg    1371
Ala Thr Gly Gly Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg
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343

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ggc ctt ggg tcg gag ctg agt aag cct ggc gtg ctg gca tcc cag gta    1419
Gly Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val
        415             420             425

gac agc ccg ttc tcg ggc tgc ttc gag gat ctt gcc atc agt gcc agc    1467
Asp Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser
    430             435             440

acc tcc ttg ggc atg ggg ccc tgc cat ggc cca gag gag aat gag tat    1515
Thr Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr
445             450             455             460

aag tcc gag ggc acc ttt ggg atc cac gtg gct gag aac ccc agc atc    1563
Lys Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile
                465             470             475

cag ctc ctg gag ggc aac cct ggg cca cct gcg gac ccg gat ggc ggc    1611
Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly
            480             485             490

ccc agg cca caa gcc gac cgg aag ttc cag gag agg gag gtg cca tgc    1659
Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys
        495             500             505

cac agg ccc tca cct ggg gct ctg tgg ctc cag gtg gct gtg aca ggg    1707
His Arg Pro Ser Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly
        510             515             520

gtg ctg gta gtc aca ctc ctg gtg gtg ctg tac cgg cgg cgt ctg cac    1755
Val Leu Val Val Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
525             530             535             540

tagtgaagcc ctgggctctt cccaccaccc atctgttccg ttcctgcagt atacctggcc    1815

cctctccgaa gcccctcttt ccctcccctc tggtctccat tctcttcagc tccctacatg    1875

ggctggggag gagacacctg gtgggcagag ctcaggcaga ggtttggatt tcagctccct    1935

cacttccggg gctgtgtggc tttggcagat gtcagacttc tggtcttgct tctccacgtg    1995

gacagtgagt atctggctca ttcttcactg ggttcttctg agattgaacc tacaggtgtt    2055

tgccaagtgc ctggcccaga gcaagtggcc actgcttctc ccatctctct cctgcccaac    2115

ctggtagagc tgagggcatg agaggcagag tgcacagtgg tcaagggtgc agctctgcgg    2175

cacaggcagc ctaggcctgc gtcccaacct gcctctcacc agctctgtga ccttgggcaa    2235

gggatttatc tgtctgtccc ttagttttct cacctgtaaa aggaggataa gtatatatat    2295

atatttccca gtgttgtgaa gattaaagga gtttatcgat gtaggtctta ggatgagtcc    2355

tggcatttac caagggttgg atatatgtta ttatcactat taagtgttga gggtccaggc    2415

atgctgggca acagggaccc catctctaca aaaaagttta aaaaattagc caggcgtggt    2475
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344

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ggtgcacctg tcgtcttagc tacttgggag gctgaggtgg gaggatcgct tgagcccgga 2535

agcttgaagc tgcagtgagc taggatcgtg ccactgcact ccaacctggg tgagagagcg 2595

agaccctgtc tcaagaaaaa gaaaaatgca gagaaacagg agtcttggct actcctttag 2655

aggcagactc agaccctcct gcctcacagc tttatctttg tatttgcccc ttactttatc 2715

ttgtgccttg agaaattgct ggggagagag gtatgtccac tgggcagctg tacaggatgg 2775

aggatatagg gcgtttccac tcccagcagc caggttccct caccccaagc tcacccactg 2835

ttggggagat tatctacaat aacaccagaa acacattggg gtggattggg ggtatcctta 2895

tgggttcttt tcagggaacc attgctggac aaggcacagg agccacctcc atttctgagc 2955

tctgcaaggg acaagaacta gagccatcag gggctgggct cactgtggcc ccaccccaag 3015

ccgtcagcct ccagggatct acaccctgcc ttggctgcta cagctttttc actccactgc 3075

cctaggggag ttcagcaacc taatgatctc tatctctgaa catctcttca tcccatgctc 3135

caagtccagc aacctgcacc ctggaaccag gagtggaccc tacccgggct gtctgtatta 3195

atccccatcc cccaccacca atcttaaaaa gccctctgtc cccctaccct aaaccccagt 3255

taggtaccca tgctgggcag gtcagttaac aatttatgca caggtactag ttttattgta 3315

ttaccgttcc agggtagctt tg                                        3337


<210> 170
<211> 540
<212> PRT
<213> Homo sapiens

<400> 170
Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe
1               5                   10                  15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
                20                  25                  30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
            35                  40                  45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
    50                  55                  60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
65                  70                  75                  80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln
                85                  90                  95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu


345
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Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
    115   120   125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
130   135   140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145   150   155   160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
          165   170   175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser
          180   185   190

Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala
          195   200   205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser
          210   215   220

Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu
225   230   235   240

Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser
          245   250   255

Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly
          260   265   270

Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu
          275   280   285

Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro
          290   295   300

Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser
305   310   315   320

Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val
          325   330   335

Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn
          340   345   350

Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val
          355   360   365

Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg
          370   375   380

Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly
385   390   395   400

Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser

346

Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe
        420   425   430

Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly
        435   440   445

Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly
    450   455   460

Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu
465   470   475   480

Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln
                485   490   495

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser
        500   505   510

Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val
        515   520   525

Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
    530   535   540

<210> 171
<211> 3579
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (242)..(3094)

<400> 171
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gaggcccgag gcggaagtgg gacggccaag cagggaagcg agggctcggg atcgacggcc 120

gcggggcgcc gacgaggagt gcaggactca ggaagggcga gtgcgcggcg acagagcccg 180

gggaaggagg cagggcaagg ccgggcttgg gggcaggtgg tccgggcatc agccttgaa 240

g atg cac aag agg aaa gga ccc ccg gga ccc ccg ggc aga ggc gcc gcg 289
  Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala
  1   5   10   15

gcc gcc cgc cag ctg ggc ctg ctg gtt gac ctc tcc cca gat ggc ctg   337
Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu
            20   25   30

atg atc cct gag gac ggg gct aac gat gaa gaa ctg gag gct gag ttc   385
Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe
        35   40   45

347

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ttg gct ttg gtc ggg ggc cag ccc cca gcc ctg gag aag ctc aaa ggc    433
Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly
         50                  55                  60

aaa ggt ccc ttg ccg atg gag gcc att gag aag atg gcc agc ctg tgc    481
Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys
 65                  70                  75                  80

atg aga gac ccg gat gag gat gag gag gag ggg acg gat gag gac gac    529
Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp
                 85                  90                  95

ttg gag gct gat gat gac ctg ctg gcg gag cta aat gag gtc ctt gga    577
Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly
                100                 105                 110

gag gag cag aag gct tca gag acc cca cct cct gtg gcc cag ccg aag    625
Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys
            115                 120                 125

cct gag gcc cct cat ccg ggg ctg gag acc acc ttg cag gag agg ctg    673
Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu
        130                 135                 140

gcg ctc tat cag aca gca att gaa agc gcc aga caa gct gga gac agc    721
Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser
145                 150                 155                 160

gcc aag atg cgg cgc tac gat cgg ggg ctt aaa aca ctg gaa aac ctg    769
Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu
                165                 170                 175

ctc gcc tcc atc cgt aag ggc aat gcc att gac gaa gcg gac atc ccg    817
Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro
                180                 185                 190

ccg cca gtg gcc ata gga aaa ggc ccg gcg tcc acg cct acc tac agc    865
Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser
            195                 200                 205

cct gca ccc acc cag ccg gcc cct aga atc gcg tca gcc cca gag ccc    913
Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro
        210                 215                 220

agg gtc acc ctg gag gga cct tct gcc acc gcc cca gcc tca tct cca    961
Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro
225                 230                 235                 240

ggc ttg gct aag ccc cag atg ccc cca ggt ccc tgc agc cct ggc cct   1009
Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro
                245                 250                 255

ctg gcc cag ttg cag agc cgc cag cgc gac tac aag ctg gct gcc ctc   1057
Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu
                260                 265                 270

cac gcc aag cag cag gga gat acc act gct gcc gct aga cac ttc cgc   1105
```

348

```
His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg
        275                 280                 285

gtg gct aag agc ttt gat gct gtc ttg gag gcc ctg agc cgg ggt gag    1153
Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu
        290                 295                 300

ccc gtg gac ctc tcc tgc ctg ccc cct cca ccc gac cag ctg ccc cca    1201
Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Asp Gln Leu Pro Pro
305                 310                 315                 320

gac cca ccg tca cca ccg tcg cag cct ccg acc ccc gct acg gcg ccc    1249
Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro
                325                 330                 335

tcc aca aca gag gtg ccc cca ccc ccg agg acc ctg ctg gag gcg ctg    1297
Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu
                340                 345                 350

gag cag cgg atg gag cgg tac cag gtg gcc gca gcc cag gcc aag agc    1345
Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser
            355                 360                 365

aag ggg gac cag cgg aaa gct cga atg cac gag cgc atc gtc aag caa    1393
Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln
        370                 375                 380

tac caa gat gcc atc cga gcc cac aag gct ggc cga gcc gtg gat gtc    1441
Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val
385                 390                 395                 400

gct gaa ttg ccc gtg ccc cca ggc ttc ccc cca atc cag ggc ctg gag    1489
Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu
                405                 410                 415

gcc acc aag ccc acc cag cag agt ctg gtg ggt gtc ctg gag act gcc    1537
Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala
                420                 425                 430

atg aag ctg gcc aac cag gat gaa ggc cca gag gat gaa gag gat gag    1585
Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu
        435                 440                 445

gtg cct aag aag cag aac agc cct gtg gcc ccc aca gcc cag ccc aaa    1633
Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys
        450                 455                 460

gcc cca ccc tca aga act ccc cag tcg gga tca gcc cca aca gcc aaa    1681
Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys
465                 470                 475                 480

gcg ccc ccc aaa gcc aca tcc acc aga gcc cag cag cag ctg gcc ttc    1729
Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe
                485                 490                 495

cta gag ggc cgc aag aag cag ctc ctg cag gcc gca ctg cga gcc aag    1777
Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys
```

349

```
cag aaa aac gac gtg gag ggt gcc aag atg cac ctg cgc caa gcc aag    1825
Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys
        515                 520                 525

gga ctg gag cct atg ctg gag gcc tcg cgc aat ggg ctg cct gtg gac    1873
Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp
        530                 535                 540

atc acc aag gtg ccg cct gcc cct gtc aac aag gac gac ttt gcc ctg    1921
Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu
545                 550                 555                 560

gtc cag cgg cct ggc ccg ggt ctg tct cag gag gcc gcc cgg cgc tat    1969
Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr
                565                 570                 575

ggt gaa ctc acc aag ctc ata cgg cag cag cac gag atg tgc ctg aac    2017
Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn
        580                 585                 590

cac tca aac caa ttc acc cag ctg ggc aac atc act gaa acc acc aag    2065
His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys
        595                 600                 605

ttt gaa aag ttg gcg gag gac tgt aag cgg agc atg gac att ctg aag    2113
Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys
        610                 615                 620

caa gcc ttc gtc cgg ggt ctc ccc acg ccc acc gcc cgc ttt gag caa    2161
Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln
625                 630                 635                 640

agg acc ttc agc gtc atc aag atc ttc cct gac ctc agc agc aac gac    2209
Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp
                645                 650                 655

atg ctc ctc ttc atc gtg aag ggc atc aac ttg ccc aca ccc cca gga    2257
Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly
                660                 665                 670

ctg tcc cct ggc gat ctg gat gtc ttt gtt cgg ttt gac ttc ccc tat    2305
Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr
        675                 680                 685

ccc aac gtg gaa gaa gct cag aaa gac aag acc agt gtg atc aag aac    2353
Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn
        690                 695                 700

aca gac tcc cct gag ttc aag gag cag ttc aaa ctc tgc atc aac cgc    2401
Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg
705                 710                 715                 720

agc cac cgt ggc ttc cga agg gcc atc cag acc aag ggc atc aag ttc    2449
Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe
                725                 730                 735
```

```
gaa gtg gtt cac aag ggg ggg ctg ttc aag act gac cgg gtg ctg ggg    2497
Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly
            740                 745                 750

aca gcc cag ctg aag ctg gat gca ctg gag ata gca tgt gag gtc cgg    2545
Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg
        755                 760                 765

gag atc ctt gag gtc ctg gat ggt cgc cgg ccc aca ggg ggg cga ctg    2593
Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu
        770                 775                 780

gag gta atg gtc cgg att cgg gag cca ctg aca gcc cag cag ttg gag    2641
Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu
785                 790                 795                 800

acg acg aca gag agg tgg ctg gtc att gac cct gtg ccg gca gct gtg    2689
Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val
                805                 810                 815

ccc aca cag gtt gct ggg ccc aaa ggg aag gcc cct cct gtg cct gcc    2737
Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala
                820                 825                 830

cct gca agg gag tca ggg aac aga tca gcc cgg ccc ctg cat agc ctc    2785
Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu
        835                 840                 845

agt gtg ctg gcg ttt gac caa gag cgt ctg gag cgg aag atc ctg gcc    2833
Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala
        850                 855                 860

ctc agg cag gcg cgg cgg ccg gtg ccc cca gaa gtg gcc cag cag tac    2881
Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr
865                 870                 875                 880

cag gac atc atg caa cgc agc cag tgg cag agg gca cag ctg gag cag    2929
Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln
                885                 890                 895

ggg ggt gtg ggc atc cga cgg gaa tac aca gcc cag ctg gag cgg cag    2977
Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln
                900                 905                 910

ctg cag ttc tac acg gag gct gcc cgg cgc ctg ggc aac gat ggc agc    3025
Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser
        915                 920                 925

agg gat gct gca aag gag gcg ctc tat agg cgg aat ctg gta ggg agt    3073
Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser
        930                 935                 940

gag ctg cag cgg ctc cgc agg tgaggagccc atggggcggg cagcccccag       3124
Glu Leu Gln Arg Leu Arg Arg
945                 950
```

351

```
aaagcgggca gcaggccccg ataccgggaa gagccgacac agccacgaac cagacaagca 3184

gacaatcagc ggacaatcgg ttctggactc acccctcatc cgggccccca gccccgccag 3244

agcctccgtg gctgcgggtg ttgggaacca tgcctgccag ccagtatgtg cccctcaccc 3304

aggcctggct gggccctgga gagtcctgtt tgcacagccc aggggtgtcc ggcctctggc 3364

ccgccccgga gcagggaggg cggctggggc caagccccga gggcccctgc aagcacttta 3424

cttcctgttc ctccccagcc ttaaccccaa agccctcctg caccccaaag aagccactga 3484

ggctggccga gccacactgt ctccccaggg gcgtcgacct ggcccagctg ggtccccagg 3544

ccagcacatg gaataaaata gccagggcca cactc                            3579
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<210> 172
<211> 951
<212> PRT
<213> Homo sapiens

<400> 172

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Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala
 1               5                  10                  15

Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu
            20                  25                  30

Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe
            35                  40                  45

Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly
     50                  55                  60

Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys
 65                  70                  75                  80

Met Arg Asp Pro Asp Glu Asp Glu Glu Gly Thr Asp Glu Asp Asp
                85                  90                  95

Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly
            100                 105                 110

Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Val Ala Gln Pro Lys
            115                 120                 125

Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu
     130                 135                 140

Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser
145                 150                 155                 160

Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu
                165                 170                 175

Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro
```

352

Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser
        195   200   205

Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro
    210   215   220

Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro
225   230   235   240

Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro
            245   250   255

Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu
            260   265   270

His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg
            275   280   285

Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu
        290   295   300

Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Asp Gln Leu Pro Pro
305   310   315   320

Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro
            325   330   335

Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu
        340   345   350

Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser
        355   360   365

Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln
    370   375   380

Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val
385   390   395   400

Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu
            405   410   415

Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala
            420   425   430

Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu
        435   440   445

Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys
    450   455   460

Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys
465   470   475   480

Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe

353

Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys
            500   505   510

Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys
            515   520   525

Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp
            530   535   540

Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu
545   550   555   560

Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr
            565   570   575

Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn
            580   585   590

His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys
            595   600   605

Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys
            610   615   620

Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln
625   630   635   640

Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp
            645   650   655

Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly
            660   665   670

Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr
            675   680   685

Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn
            690   695   700

Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg
705   710   715   720

Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe
            725   730   735

Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly
            740   745   750

Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg
            755   760   765

Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu
            770   775   780

Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu

354

Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val
            805   810   815

Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala
            820   825   830

Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu
            835   840   845

Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala
    850   855   860

Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr
865   870   875   880

Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln
            885   890   895

Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln
            900   905   910

Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser
            915   920   925

Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser
    930   935   940

Glu Leu Gln Arg Leu Arg Arg
945   950

<210> 173
<211> 2796
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<220>
<221> CDS
<222> (574)..(1683)

<400> 173
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tagtccttaa caaagggaaa gcgataaatg taaataagct cacattttca gaatgagcgg 180

tttgcagtaa ggagctgcgg cagcccagag tctgctcttt ttgggctggg ctaacctttc 240

cctgtttttt gttttttgtt ttgttttgtt tttgtttttt atggataaaa atatgcgctt 300

ccgaagtgcg agttgccagt ttacacgttt attagctaac tatctacagg catgagcaca 360

ttctctcatc tagcacactc tttcttgggc actcaattga ggaactctct gatcgtctgc 420

ctccagaaaa ttcattgatt atccaagtct cagataaatc tggtgccaga gtttggtttg 480

aactaactaa tgaagaaagc attctctact ggtcctcagt ctcaagagtg gtgaacccct 540

gcacctagca ggctctctgg gaaaaaaaaa tcc atg ggt gac aga aga ttt att 594
                                     Met Gly Asp Arg Arg Phe Ile
                                      1   5

gac ttc caa ttc caa gat tta aat tca agt ctc aga ccc agg ttg gga 642
Asp Phe Gln Phe Gln Asp Leu Asn Ser Ser Leu Arg Pro Arg Leu Gly
          10   15   20

aat gca act gcc aat aat act tgc att gtt gat gat tcc ttc aag tat 690
Asn Ala Thr Ala Asn Asn Thr Cys Ile Val Asp Asp Ser Phe Lys Tyr
      25   30   35

aat ttg aat ggt gct gtc tat agt gtt gta ttc atc ctg ggt cta ata 738
Asn Leu Asn Gly Ala Val Tyr Ser Val Val Phe Ile Leu Gly Leu Ile
 40   45   50   55

acc aac agt gcc tcc ctg ttt gtc ttc tgc ttc cgc atg aaa atg aga 786
Thr Asn Ser Ala Ser Leu Phe Val Phe Cys Phe Arg Met Lys Met Arg
              60   65   70

agt gag acg gct act ttc atc acc aac ctg gcc ctc tct gat ttg ctt 834
Ser Glu Thr Ala Thr Phe Ile Thr Asn Leu Ala Leu Ser Asp Leu Leu
              75   80   85

ttt gtt tgt acc cta cct ttc aaa ata ttt tac aac ttt aat cgc cac 882
Phe Val Cys Thr Leu Pro Phe Lys Ile Phe Tyr Asn Phe Asn Arg His
              90   95   100

tgg cct ttt ggt gac acc ctc tgt aag atc tca ggg act gcg ttc ctc 930
Trp Pro Phe Gly Asp Thr Leu Cys Lys Ile Ser Gly Thr Ala Phe Leu
 105   110   115

acc aac atc tat ggg agc atg ctc ttc ctc acc tgc atc agt gtg gat 978
Thr Asn Ile Tyr Gly Ser Met Leu Phe Leu Thr Cys Ile Ser Val Asp
120   125   130   135

cgt ttc cta gcc att gtc tat ccc ttc cga tcg cgt acc atc agg acc 1026
Arg Phe Leu Ala Ile Val Tyr Pro Phe Arg Ser Arg Thr Ile Arg Thr
                140   145   150

agg agg aat tcc gcc att gtg tgc gct gga gtc tgg atc cta gtc ctc 1074
Arg Arg Asn Ser Ala Ile Val Cys Ala Gly Val Trp Ile Leu Val Leu
              155   160   165

agt ggt ggt att tca gct tct ttg ttc tcc acc act aat gtc aac aat 1122
Ser Gly Gly Ile Ser Ala Ser Leu Phe Ser Thr Thr Asn Val Asn Asn
              170   175   180

gcg acc acc act tgc ttt gaa ggc ttc tcc aaa cgt gtc tgg aag aca 1170
Ala Thr Thr Thr Cys Phe Glu Gly Phe Ser Lys Arg Val Trp Lys Thr
      185   190   195

tac ctg tcc aag atc act ata ttc att gaa gtt gtt gga ttc atc att 1218

356

```
-Tyr Leu Ser Lys Ile Thr Ile Phe Ile Glu Val Val Gly Phe Ile Ile
200           205           210           215


cct ctg ata ttg aat gtt tct tgt tct tct gtg gtg ctt aga acc ctc   1266
Pro Leu Ile Leu Asn Val Ser Cys Ser Ser Val Val Leu Arg Thr Leu
                220           225           230


cgc aag cct gca aca ttg tct cag att ggg acc aat aag aaa aaa gtg   1314
Arg Lys Pro Ala Thr Leu Ser Gln Ile Gly Thr Asn Lys Lys Lys Val
            235           240           245


ttg aag atg atc aca gtg cat atg gca gtg ttt gtg gta tgc ttt gta   1362
Leu Lys Met Ile Thr Val His Met Ala Val Phe Val Val Cys Phe Val
            250           255           260


cca tac aac tcc gtt ctc ttt tta tat gcc ttg gta cgc tcc caa gcc   1410
Pro Tyr Asn Ser Val Leu Phe Leu Tyr Ala Leu Val Arg Ser Gln Ala
            265           270           275


att act aat tgc tta ttg gaa agg ttt gca aag atc atg tac cca att   1458
Ile Thr Asn Cys Leu Leu Glu Arg Phe Ala Lys Ile Met Tyr Pro Ile
280           285           290           295


acc ttg tgc ctt gca act ctg aat tgt tgc ttt gat cct ttt atc tat   1506
Thr Leu Cys Leu Ala Thr Leu Asn Cys Cys Phe Asp Pro Phe Ile Tyr
                300           305           310


tac ttc act ctt gaa tcc ttt cag aag tcc ttt tat atc aat aca cat   1554
Tyr Phe Thr Leu Glu Ser Phe Gln Lys Ser Phe Tyr Ile Asn Thr His
            315           320           325


ata agg atg gag tcg ctg ttt aag act gag aca cct ctg acc ccc aaa   1602
Ile Arg Met Glu Ser Leu Phe Lys Thr Glu Thr Pro Leu Thr Pro Lys
            330           335           340


cct tcc ctt cca gct atc caa gag gaa gtt agt gat caa aca aca aat   1650
Pro Ser Leu Pro Ala Ile Gln Glu Glu Val Ser Asp Gln Thr Thr Asn
345           350           355


aat ggt ggt gaa tta atg ctg gaa tcc acc ttc taggtaccag aattgtcttt 1703
Asn Gly Gly Glu Leu Met Leu Glu Ser Thr Phe
360           365           370


caggttcagc tacagtgtct cttatgattt ttttcctatg ctataaatag gagaaacaaa 1763

ttgaagctaa tgatactgag aatagagtaa tgtaccaaat gcagtcagat acatttgttt 1823

gaacactatt gtacatattc tgttttgttc agtaattata ggtcaagtct aattacaaca 1883

accaaaacag atcagcctct tctgttgagt tgacttttca ttacctaaat gaccagtggt 1943

cttgactttt agtgatgtga gggttatttt taaacttaaa aaaaaaggca ttccagtaat 2003

tttggtaatt gggttgggcc tataaatata gaacaaattc aggggattatt taaaaacatc 2063

tgtgttacta ctgatatatg ctagtatttt tttcctttttt tgaattaata ttgaatttat 2123
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357

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tttaaaaaaa gaactatttt tacctaatct taataagaca tactgagaaa-gagaaatgtg 2183

ttgaatttta aaatattggc aaattttacc tagattttaa aaacctaaat gaagtgtttg 2243

aatgaatatg ggtgggaaat ttggaattta gacaacattt acgcatttat aataaccaca 2303

attagtgtca gcttttaaaa ctttcttttt aaaataattc tagaattttc atatgaaatt 2363

gttaatcctg aaaggtgcta cttatgtgcc tggcaggtat aaaatggaaa actcataaaa 2423

ttaacagtgt caatttaaaa aaaaaaaaac tttaagcaac actatattat ttcttaagat 2483

tttcatttat cctttatggg ggtgggggatt ggcttgtaga aaatatttat tcttcatgtt 2543

aaatgttggg gacacattac agccagagag ctacagtatt tgtgcccagg tcaggagtaa 2603

attgaaaaag taagtgaata gaatagtagc agcaagatat cttagagctt atattagtag 2663

tttttaaggt ggtggttaga tagctgtaat tttgaaatcc atactctctt ctgtacattt 2723

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aagatgtgta cat                                                    2796
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<210> 174
<211> 370
<212> PRT
<213> Mus musculus

<400> 174

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Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Leu Asn Ser
 1               5                   10                  15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile
            20                  25                  30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val
        35                  40                  45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Ala Ser Leu Phe Val Phe
    50                  55                  60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Thr Phe Ile Thr Asn
65                  70                  75                  80

Leu Ala Leu Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
                85                  90                  95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys
                100                 105                 110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
            115                 120                 125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
    130                 135                 140
```

358

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala
145   150   155   160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe
            165   170   175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe
            180   . 185   190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile
            195   200   205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
            210   215   220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
225   230   235   240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
            245   250   255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
            260   265   270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Leu Leu Glu Arg Phe
            275   280   285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
            290   295   300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
305   310   . 315   320

Ser Phe Tyr Ile Asn Thr His Ile Arg Met Glu Ser Leu Phe Lys Thr
            325   330   335

Glu Thr Pro Leu Thr Pro Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
            340   345   350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser
            355   360   365

Thr Phe
    370

<210> 175
<211> 2299
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (67)..(1176)

<400> 175

359

cctaccggtc catagtgtca gagtggtgaa cccctgcagc cagcaggcct cctgaaaaaa 60

```
aagtcc atg ggt gac aga aga ttc att gac ttc caa ttc caa gat tca   108
       Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser
        1               5                   10
```

```
aat tca agc ctc aga ccc agg ttg ggc aat gct act gcc aat aat act   156
Asn Ser Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr
 15                 20                  25                  30
```

```
tgc att gtt gat gat tcc ttc aag tat aat ctc aat ggt gct gtc tac   204
Cys Ile Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr
                35                  40                  45
```

```
agt gtt gta ttc atc ttg ggt ctg ata acc aac agt gtc tct ctg ttt   252
Ser Val Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe
                50                  55                  60
```

```
gtc ttc tgt ttc cgc atg aaa atg aga agt gag act gct att ttt atc   300
Val Phe Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile
            65                  70                  75
```

```
acc aat cta gct gtc tct gat ttg ctt ttt gtc tgt aca cta cct ttt   348
Thr Asn Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe
         80                  85                  90
```

```
aaa ata ttt tac aac ttc aac cgc cac tgg cct ttt ggt gac acc ctc   396
Lys Ile Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu
 95                 100                 105                 110
```

```
tgc aag atc tct gga act gca ttc ctt acc aac atc tat ggg agc atg   444
Cys Lys Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met
                115                 120                 125
```

```
ctc ttt ctc acc tgt att agt gtg gat cgt ttc ctg gcc att gtc tat   492
Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr
                130                 135                 140
```

```
cct ttt cga tct cgt act att agg act agg agg aat tct gcc att gtg   540
Pro Phe Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val
            145                 150                 155
```

```
tgt gct ggt gtc tgg atc cta gtc ctc agt ggc ggt att tca gcc tct   588
Cys Ala Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser
    160                 165                 170
```

```
ttg ttt tcc acc act aat gtc aac aat gca acc acc acc tgc ttt gaa   636
Leu Phe Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu
175                 180                 185                 190
```

```
ggc ttc tcc aaa cgt gtc tgg aag act tat tta tcc aag atc aca ata   684
Gly Phe Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile
                195                 200                 205
```

```
ttt att gaa gtt gtt ggg ttt atc att cct cta ata ttg aat gtc tct   732
Phe Ile Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser
                210                 215                 220
```

360

```
tgc tct tct gtg gtg ctg aga act ctt cgc aag cct gct act ctg tct    780
Cys Ser Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser
        225                 230                 235

caa att ggg acc aat aag aaa aaa gta ctg aaa atg atc aca gta cat    828
Gln Ile Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His
        240                 245                 250

atg gca gtc ttt gtg gta tgc ttt gta ccc tac aac tct gtc ctc ttc    876
Met Ala Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe
255                 260                 265                 270

ttg tat gcc ctg gtg cgc tcc caa gct att act aat tgc ttt ttg gaa    924
Leu Tyr Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu
                275                 280                 285

aga ttt gca aag atc atg tac cca atc acc ttg tgc ctt gca act ctg    972
Arg Phe Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu
                290                 295                 300

aac tgt tgt ttt gac cct ttc atc tat tac ttc acc ctt gaa tcc ttt   1020
Asn Cys Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe
            305                 310                 315

cag aag tcc ttc tac atc aat gcc cac atc aga atg gag tcc ctg ttt   1068
Gln Lys Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe
        320                 325                 330

aag act gaa aca cct ttg acc aca aag cct tcc ctt cca gct att caa   1116
Lys Thr Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln
335                 340                 345                 350

gag gaa gtg agt gat caa aca aca aat aat ggt ggt gaa tta atg cta   1164
Glu Glu Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu
                355                 360                 365

gaa tcc acc ttt taggtatgag aaatgtgttc aggtccagat atggtttctc       1216
Glu Ser Thr Phe
            370

ctataatttt tcctatgcta taaactaaag atttgaagct aatgatactg agaataatgc 1276

accaaatcca gtcagataca tttgtttgaa ggtatactgt agagttttta ttgctgtttt 1336

gttcagtaat tataggtcaa atctaattac aacaaccaag atggattgcc aaactcttct 1396

gcttggttgg aatttcattg tatcgcatta tccaggtggc tagtggcatt tgataatata 1456

gagatgactt tgaaactttc aaaaaggtat ttctattcca atgatatttg gtaattaggt 1516

tgggcctata aatatagaac aaattcaggg attttttaaaa aattgtgtta ctactgatat 1576

atgctagttt tattttattt ttttggactg tcattgagtt tattttagca caagaatatt 1636

tttagcctaa cattattaat aagaaatgtg tcaaattttt aacattggta aaatatgtta 1696
```

```
-tgtgcattt gaaaacagaa aacaaattgc gttggcatgt acgtgggtgg gaagaaaaag 1756

aaaattaaca ggatttacac aattataatc accagcagtg tgagtttaaa aaacttcgtt 1816

gttttacac caaattaaaa ttttcatgtc aaacttcaaa gccagaaagc tgctaaatac 1876

gtgtctggca ggtaaaagct ggaaaattac ttaaaacagg aaagtgtcaa taaaaaaact 1936

tgagcaacac caacatattt tttcttaaaa tgtcacgtta tcttcatttt gggaaactag 1996

gttctataaa atatttatcc tccctgttat actttggagc acagcacagc cagaaagggg 2056

ctgcatttgt gcccaggtca ggagcaaatt gaaaaaaaaa ataaagtaat actaaaaaat 2116

caaactataa acccaaaaca tttattaaaa cctgaattaa tcctttttgg agggaggagt 2176

agagatatat aacctgaaaa tacttattct ttcttatcga attttggagc ctaatatagc 2236

caggagctgc tgaatttgtg cccctggatt ggaaccaaat aaaaaaaaaa aaaaaaatt 2296

cct                                                          2299


<210> 176
<211> 370
<212> PRT
<213> Homo sapiens

<400> 176
Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser
  1               5                  10                  15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile
             20                  25                  30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val
         35                  40                  45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe
     50                  55                  60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn
 65                  70                  75                  80

Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
                 85                  90                  95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys
                100                 105                 110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
             115                 120                 125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
         130                 135                 140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala
```

362

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe
                165   170   175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe
                180   185   190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile
                195   200   205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
    210   215   220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
225   230   235   240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
                245   250   255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
                260   265   270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe
                275   280   285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
    290   295   300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
305   310   315   320

Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe Lys Thr
                325   330   335

Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
                340   345   350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser
    355   360   365

Thr Phe
    370

<210> 177
<211> 973
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (30)..(416)

<400> 177
cagacagcgg cgggcgcagg acgtgcact atg gct cgg ggc tcg ctg cgc cgg   53
                                 Met Ala Arg Gly Ser Leu Arg Arg

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ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg ctg gcg ttg ctg cgc tcc   101
Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser
     10              15              20

gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc   149
Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser
 25              30              35              40

tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg   197
Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg
             45              50              55

gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct   245
Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro
         60              65              70

gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg   293
Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu
     75              80              85

acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc   341
Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys
     90              95              100

cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag   389
Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu
105              110              115              120

ggc tgc cca gct gtg gcg ctg atc cag tgacaatgtg ccccctgcca   436
Gly Cys Pro Ala Val Ala Leu Ile Gln
             125
```

```
gccggggctc gcccactcat cattcattca tccattctag agccagtctc tgcctcccag 496

acgcggcggg agccaagctc ctccaaccac aaggggggtg ggggcggtg aatcacctcc 556

gaggcctggg tccagggttc aggggaacct ccaaggtgt ctggttgccc tgcctctggc 616

tccagaacag aaagggagcc tcacgctggc tcacacaaaa cagctgacac tgactaagga 676

actgcagcat ttgcacaggg gagggggtg ccctccttcc tagaggccct ggggggccagg 736

ctgacttggg gggcagactt gacactaggc cccactcact cagatgtcct gaaattccac 796

cacgggggtc accctggggg gttagggacc tatttttaac actaggggc tggcccacta 856

ggagggctgg ccctaagata cagaccccccc caactccccca aagcggggag gagatattta 916

ttttggggag agtttggagg ggaggagaa tttattaata aaagaatctt taacttt   973
```

<210> 178
<211> 129
<212> PRT
<213> Homo sapiens

<400> 178
Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
1   5   10   15

Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
            20   25   30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
            35   40   45

Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
        50   55   60

Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
65   70   75   80

Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
            85   90   95

Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Glu Lys Phe Thr Thr
            100   105   110

Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
        115   120   125

Gln

<210> 179
<211> 3631
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (191)..(3244)

<400> 179
tctaaatcag cggccgctga attctagggc gctgctggcg ctgcagctgc acttgctccg 60

ggcgctggcg caagatgatg ttgctccata ttttaaaacg gagccaggcc taccacagat 120

ccacctggaa gggaaccgcc ttgttctcac ctgccttgcc gaagggagct ggcctttgga 180

gttcaagtgg atg cgc gat gac agt gag ctc acc acc tac agc agc gaa   229
              Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu
              1   5   10

tat aag tac att att cca tct ttg cag aag ctc gat gct ggg ttt tac   277
Tyr Lys Tyr Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr
        15   20   25

cgc tgc gtg gtg cga aac aga atg gga gca ctc ctg caa aga aaa tca   325
Arg Cys Val Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser
30   35   40   45

```
gaa gtt caa gtc gca tat atg gga agt ttc atg gat acg gac cag agg      373
Glu Val Gln Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg
            50                  55                  60

aaa aca gtt tct caa gga cgt gca gcg att cta aac ctg ctg ccc atc      421
Lys Thr Val Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile
            65                  70                  75

acc agc tac ccc aga cct caa gtg act tgg ttt aga gaa ggg cac aag      469
Thr Ser Tyr Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys
            80                  85                  90

att att cca agc aac aga ata gcc atc aca ttg gag aat cag ctg gtg      517
Ile Ile Pro Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val
        95                  100                 105

atc ctc gcc acc aca acc agt gat gcc ggg gca tac tac gtg cag gcc      565
Ile Leu Ala Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala
110                 115                 120                 125

gtg aat gag aaa aat gga gaa aac aag aca agc cca ttc att cat ttg      613
Val Asn Glu Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu
                130                 135                 140

agc ata gca aga gat gtt ggc aca cct gaa acc atg gcc cca acc att      661
Ser Ile Ala Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile
            145                 150                 155

gtg gtt ccc ccg ggc aac aga agt gtg gtg gct gga tcc agt gag acc      709
Val Val Pro Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr
            160                 165                 170

acc ttg gaa tgt ata gcc agt gcc agg cct gtg gag gac ctg agt gtg      757
Thr Leu Glu Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val
            175                 180                 185

acc tgg aag agg aat gga gtg aga atc acc agt ggc ctc cac agc ttt      805
Thr Trp Lys Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe
190                 195                 200                 205

gga aga cgc ctc acc atc agc aac ccg acg tcc gcg gac acc ggg cca      853
Gly Arg Arg Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro
                210                 215                 220

tac gtc tgc gag gcg gcg ctg ccg ggg agc gct ttt gaa ccg gcc agg      901
Tyr Val Cys Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg
            225                 230                 235

gcg acg gcc ttt ctt ttc atc ata gag cca cca tat ttt act gct gag      949
Ala Thr Ala Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu
            240                 245                 250

ccc gag agt cgg att tca gct gaa gta gaa gaa act gtg gac atc gga      997
Pro Glu Ser Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly
        255                 260                 265
```

366

```
-tgt caa gcc atg ggg gtc ccc ctt ccc acc ctc cag tgg tac aag gat    1045
 Cys Gln Ala Met Gly Val Pro Leu Pro Thr Leu Gln Trp Tyr Lys Asp
 270             275             280             285

 gcc atc tcc atc agc agg ctc cag aat cct cga tac aaa gtg ctc gcc    1093
 Ala Ile Ser Ile Ser Arg Leu Gln Asn Pro Arg Tyr Lys Val Leu Ala
             290             295             300

 agc gga ggc ctg cgc atc cag aag ctg cgt cca gag gac tcc gga atc    1141
 Ser Gly Gly Leu Arg Ile Gln Lys Leu Arg Pro Glu Asp Ser Gly Ile
             305             310             315

 ttc cag tgc ttc gcc agc aat gaa gga ggg gag atc cag acc cac acc    1189
 Phe Gln Cys Phe Ala Ser Asn Glu Gly Gly Glu Ile Gln Thr His Thr
             320             325             330

 tac ctg gat gta acc aat atc gct cca gtg ttc acc cag cgg cca gtg    1237
 Tyr Leu Asp Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val
             335             340             345

 gac acc aca gtt act gac ggg atg aca gcc att cta agg tgt gag gtg    1285
 Asp Thr Thr Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val
 350             355             360             365

 tcc ggg gct ccc aaa ccc gcc atc acc tgg aaa aga gaa aac cac att    1333
 Ser Gly Ala Pro Lys Pro Ala Ile Thr Trp Lys Arg Glu Asn His Ile
             370             375             380

 ctg gcc agt ggc tct gtc cgg att cct agg ttc atg ctt ctt gaa tcg    1381
 Leu Ala Ser Gly Ser Val Arg Ile Pro Arg Phe Met Leu Leu Glu Ser
             385             390             395

 ggg ggt cta cag atc gcg ccc gtc ttc atc cag gat gcc ggc aac tac    1429
 Gly Gly Leu Gln Ile Ala Pro Val Phe Ile Gln Asp Ala Gly Asn Tyr
             400             405             410

 acc tgc tat gcg gcc aac aca gag ggc tcc ctg aat gca tcg gcc acg    1477
 Thr Cys Tyr Ala Ala Asn Thr Glu Gly Ser Leu Asn Ala Ser Ala Thr
             415             420             425

 ctc act gtg tgg aat cgg acg tcc atc gtc cac cct cct gag gac cac    1525
 Leu Thr Val Trp Asn Arg Thr Ser Ile Val His Pro Pro Glu Asp His
 430             435             440             445

 gtg gtg att aag ggg acc acg gcc acg ctg cac tgt ggt gcc aca cat    1573
 Val Val Ile Lys Gly Thr Thr Ala Thr Leu His Cys Gly Ala Thr His
             450             455             460

 gac ccc cgg gtt tca ctc cgc tac gtt tgg aag aag gac aac gtg gcc    1621
 Asp Pro Arg Val Ser Leu Arg Tyr Val Trp Lys Lys Asp Asn Val Ala
             465             470             475

 ctg act cca tcg agc acg tct agg atc gtg gtg gag aag gac ggg tcc    1669
 Leu Thr Pro Ser Ser Thr Ser Arg Ile Val Val Glu Lys Asp Gly Ser
             480             485             490

 ctt ctc atc agc cag acg tgg tca ggc gac atc ggt gac tac agc tgc    1717
```

367

```
Leu Leu Ile Ser Gln Thr Trp Ser Gly Asp Ile Gly Asp Tyr Ser Cys
    495                 500                 505

gag att gtt tct gaa gga ggg aat gac tcc agg atg gcc cgg ctg gaa    1765
Glu Ile Val Ser Glu Gly Gly Asn Asp Ser Arg Met Ala Arg Leu Glu
510                 515                 520                 525

gtg att gaa ctg cct cat tca cct cag aac ctc ctg gtc agc cct aat    1813
Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn
                530                 535                 540

tct tcc cac agc cac gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat    1861
Ser Ser His Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp
                545                 550                 555

gga aac agt cct att ctt tat tac atc gtg gag ctg tct gaa aac aac    1909
Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn
                560                 565                 570

tct cca tgg aag gtg cat ctg tca aac gtt ggc cct gag atg aca ggc    1957
Ser Pro Trp Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly
    575                 580                 585

gtc acc gtg agt ggc ctg act ccg gct cgt acc tat caa ttc cgg gtg    2005
Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val
590                 595                 600                 605

tgc gcg gtg aat gaa gtg ggc agg ggc cag tac agt gcc gag aca agc    2053
Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser
                610                 615                 620

agg ttg atg cta cct gaa gaa cca ccc agt gct ccc ccg aaa aat ata    2101
Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile
                625                 630                 635

gtg gcc agt ggg cgg act aat cag tcc att atg gtc cag tgg cag cca    2149
Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro
                640                 645                 650

ccc cca gaa aca gag cac aac ggg gtg ttg cgt gga tac atc ctc agg    2197
Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg
    655                 660                 665

tac cgc ctg gct ggc ctt ccc gga gag tac cag cag cgg aac atc acc    2245
Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr
670                 675                 680                 685

agc ccg gag gtg aac tac tgc ctg gtg aca gac ctg atc atc tgg aca    2293
Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr
                690                 695                 700

cag tat gag ata cag gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc    2341
Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val
                705                 710                 715

ttc agc agg gca gtg acc gag tac acc ttg cag gga gtg ccc acc gcg    2389
Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala
```

368

ccc ccg cag aac gtg cag acg gaa gcc gtg aac tcc acc acc att cag   2437
Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln
    735   740   745

ttc ctg tgg aac cct ccg cct cag cag ttt atc aat ggc atc aac cag   2485
Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln
750   755   760   765

gga tac aag ctt ctg gca tgg ccg gca gat gcc ccc gag gct gtc act   2533
Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr
            770   775   780

gtg gtc act att gcc cca gat ttc cac gga gtc cac cat gga cac ata   2581
Val Val Thr Ile Ala Pro Asp Phe His Gly Val His His Gly His Ile
            785   790   795

acg aac ctg aag aag ttt acc gcc tac ttc act tcc gtt ctg tgc ttc   2629
Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe
        800   805   810

acc acc cct ggg gac ggg cct ccc agc aca cct cag ctg gtc tgg act   2677
Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr
    815   820   825

cag gaa gac aaa cca gga gct gtg gga cat ctg agt ttc aca gag atc   2725
Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile
830   835   840   845

ttg gac aca tct ctc aag gtc agc tgg cag gag ccc ctg gag aaa aat   2773
Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn
            850   855   860

ggc atc att act ggc tat cag atc tct tgg gaa gtg tac ggc agg aac   2821
Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn
            865   870   875

gac tct cgt ctc acg cac acc ctg aac agc acg acg cac gag tac aag   2869
Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys
        880   885   890

atc caa ggc ctc tca tct ctc acc acc tac acc atc gac gtg gcc gct   2917
Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala
    895   900   905

gtg act gcc gtg ggc act ggc ctg gtg act tca tcc acc att tct tct   2965
Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser
910   915   920   925

gga gtg ccc cca gac ctt cct ggt gcc cca tcc aac ctg gtc att tcc   3013
Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser
            930   935   940

aac atc agc cct cgc tcc gcc acc ctt cag ttc cgg cca ggc tat gac   3061
Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp
            945   950   955

369

```
ggg aaa acg tcc atc tcc agg tgg att gtt gag ggg cag atg aga cat      3109
Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu Gly Gln Met Arg His
        960                 965                 970

caa ggt gtt gga tta cct gcc gag gtc aca cag cca agc cat gaa gcc      3157
Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala
        975                 980                 985

gga ttg gag cct gca aac ctc gga agt ctg tgg ctg ctc agc ctg gtg      3205
Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val
990                 995                 1000                1005

tat tgg tgt tac agc cag aaa ctt tgg gaa ttc tct tgt tagttggtta      3254
Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe Ser Cys
                1010                1015

gttttactgt aattttctat aaagaattca tatcatctgt taatggcgac agtttttgtt 3314

tcttcctttg aattttttat attctttctt tctctttttt gtttcttctt ctttgagtat 3374

tttgtaatct tactgggagg gctaaagcgt cttctatcat atcgaattgg gacaatgata 3434

gaagacaatc tttgttttgt cactctaaag aaattattgt aagattttat catcaggtat 3494

gacatttaca ccattgatgt aggctttta aaaaatatat ccagcctgta ttgggttaag 3554

atgattcttt tctgatcctg atttcctagg agttggtttt tttttttta aagcataaat 3614

aaatttaatt gcatcag                                                 3631


<210> 180
<211> 1018
<212> PRT
<213> Homo sapiens

<400> 180
Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu Tyr Lys Tyr
1               5                   10                  15

Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr Arg Cys Val
                20                  25                  30

Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser Glu Val Gln
        35                  40                  45

Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg Lys Thr Val
    50                  55                  60

Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile Thr Ser Tyr
65                  70                  75                  80

Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys Ile Ile Pro
                85                  90                  95

Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val Ile Leu Ala
```

370

Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala Val Asn Glu
    115   120   125

Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu Ser Ile Ala
    130   135   140

Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile Val Val Pro
145   150   155   160

Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr Thr Leu Glu
          165   170   175

Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val Thr Trp Lys
          180   185   190

Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe Gly Arg Arg
          195   200   205

Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro Tyr Val Cys
    210   215   220

Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg Ala Thr Ala
225   230   235   240

Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu Pro Glu Ser
          245   250   255

Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly Cys Gln Ala
          260   265   270

Met Gly Val Pro Leu Pro Thr Leu Gln Trp Tyr Lys Asp Ala Ile Ser
          275   280   285

Ile Ser Arg Leu Gln Asn Pro Arg Tyr Lys Val Leu Ala Ser Gly Gly
    290   295   300

Leu Arg Ile Gln Lys Leu Arg Pro Glu Asp Ser Gly Ile Phe Gln Cys
305   310   315   320

Phe Ala Ser Asn Glu Gly Gly Glu Ile Gln Thr His Thr Tyr Leu Asp
          325   330   335

Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val Asp Thr Thr
          340   345   350

Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val Ser Gly Ala
          355   360   365

Pro Lys Pro Ala Ile Thr Trp Lys Arg Glu Asn His Ile Leu Ala Ser
    370   375   380

Gly Ser Val Arg Ile Pro Arg Phe Met Leu Leu Glu Ser Gly Gly Leu
385   390   395   400

Gln Ile Ala Pro Val Phe Ile Gln Asp Ala Gly Asn Tyr Thr Cys Tyr

Ala Ala Asn Thr Glu Gly Ser Leu Asn Ala Ser Ala Thr Leu Thr Val
420 425 430

Trp Asn Arg Thr Ser Ile Val His Pro Pro Glu Asp His Val Val Ile
435 440 445

Lys Gly Thr Thr Ala Thr Leu His Cys Gly Ala Thr His Asp Pro Arg
450 455 460

Val Ser Leu Arg Tyr Val Trp Lys Lys Asp Asn Val Ala Leu Thr Pro
465 470 475 480

Ser Ser Thr Ser Arg Ile Val Val Glu Lys Asp Gly Ser Leu Leu Ile
485 490 495

Ser Gln Thr Trp Ser Gly Asp Ile Gly Asp Tyr Ser Cys Glu Ile Val
500 505 510

Ser Glu Gly Gly Asn Asp Ser Arg Met Ala Arg Leu Glu Val Ile Glu
515 520 525

Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His
530 535 540

Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser
545 550 555 560

Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp
565 570 575

Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val
580 585 590

Ser Gly Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val
595 600 605

Asn Glu Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met
610 615 620

Leu Pro Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser
625 630 635 640

Gly Arg Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu
645 650 655

Thr Glu His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu
660 665 670

Ala Gly Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu
675 680 685

Val Asn Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu
690 695 700

Ile Gln Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg

372

Ala Val Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln
                725   730   735

Asn Val Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp
            740   745   750

Asn Pro Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys
        755   760   765

Leu Leu Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr
    770   775   780

Ile Ala Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu
785   790   795   800

Lys Lys Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro
            805   810   815

Gly Asp Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp
        820   825   830

Lys Pro Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr
        835   840   845

Ser Leu Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile
    850   855   860

Thr Gly Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg
865   870   875   880

Leu Thr His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly
            885   890   895

Leu Ser Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala
        900   905   910

Val Gly Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro
    915   920   925

Pro Asp Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser
    930   935   940

Pro Arg Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr
945   950   955   960

Ser Ile Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val
            965   970   975

Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu
        980   985   990

Pro Ala Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys
        995   1000   1005

Tyr Ser Gln Lys Leu Trp Glu Phe Ser Cys

<210> 181
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 181
cttctgctct aaaagctgcg   20

<210> 182
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 182
cgacctgcag ctcgagcaca   20

<210> 183
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 183
ctagctagct agaaactact aaaatgtaaa tgacatag   38

<210> 184
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 184
cgcaagcttg aaaggttgca gttagaatgt cctttc   36

<210> 185
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<220>
<223> DNA/RNA molecule

<400> 185
guccaggaua ucaugaguct t   21

<210> 186
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<220>
<223> DNA/RNA molecule

<400> 186
gacucaugau auccuggact t   21

<210> 187
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<220>
<223> DNA/RNA molecule

<400> 187
gaagucugaa gaucuaucct t   21

<210> 188
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<220>
<223> DNA/RNA molecule

<400> 188
ggauagaucu ucagacuuct t   21

375

<210> 189
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
    double stranded nucleic acid

<220>
<223> DNA/RNA molecule

<400> 189
gcugaagaag agguguucct t   21

<210> 190
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
    double stranded nucleic acid

<220>
<223> DNA/RNA molecule

<400> 190
ggaacaccuc uucuucagct t   21

<210> 191
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
    double stranded nucleic acid

<220>
<223> DNA/RNA molecule

<400> 191
gaugacacag augaagccct t   21

<210> 192
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
    double stranded nucleic acid

<220>
<223> DNA/RNA molecule

<400> 192
gggcuucauc ugugucauct t   21

<210> 193
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<220>
<223> DNA/RNA molecule

<400> 193
gcccucagag uccagaauct t   21

<210> 194
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<220>
<223> DNA/RNA molecule

<400> 194
gauucuggac ucgagggct t   21

<210> 195
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<220>
<223> DNA/RNA molecule

<400> 195
gaugacuuug guaucaaact t   21

<210> 196

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<220>
<223> DNA/RNA molecule

<400> 196
guuugauacc aaagucauct t   21

<210> 197
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 197
aaaagtccag gatatcatga gtctttttta   30

<210> 198
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 198
agcttaaaaa agactcatga tatcctggac   30

<210> 199
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 199
aaaagaagtc tgaagatcta tcctttttta   30

<210> 200
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<400> 200
agcttaaaaa aggatagatc ttcagacttc   30

<210> 201
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 201
aaaagctgaa gaagaggtgt tccttttta   30

<210> 202
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 202
agcttaaaaa aggaacacct cttcttcagc   30

<210> 203
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 203
aaaagatgac acagatgaag cccttttta   30

<210> 204
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 204
agcttaaaaa agggcttcat ctgtgtcatc   30

<210> 205
<211> 30
<212> DNA

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 205
aaaagccctc agagtccaga atcttttta   30

<210> 206
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 206
agcttaaaaa agattctgga ctctgagggc   30

<210> 207
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 207
aaaagatgac tttggtatca aacttttta   30

<210> 208
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic DNA

<400> 208
agcttaaaaa agtttgatac caaagtcatc   30

<210> 209
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 209
gcgaattcgg gcaggaagag ggcctatttc ccat   34

<210> 210
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 210
gcaagctttt tttgtcttct ttccacaaga tatataaagc caag   44

<210> 211
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 211
cgctcgagcc atggaattcg aacgctgacg tc   32

<210> 212
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 212
gcaagctttc tcatacagaa cttataagat tccc   34

<210> 213
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
    double stranded nucleic acid

<400> 213
guccaggaua ucaugaguc   19

<210> 214
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
    double stranded nucleic acid

<400> 214
gacucaugau auccuggac   19

<210> 215
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<400> 215
gaagucugaa gaucuaucc   19

<210> 216
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<400> 216
ggauagaucu ucagacuuc   19

<210> 217
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<400> 217
gcugaagaag agguguucc   19

<210> 218
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<400> 218
ggaacaccuc uucuucagc   19

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<210> 219
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<400> 219
gaugacacag augaagccc                                              19


<210> 220
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<400> 220
gggcuucauc ugugucauc                                              19


<210> 221
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<400> 221
gcccucagag uccagaauc                                              19


<210> 222
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<400> 222
gauucuggac ucugagggc                                              19


<210> 223
<211> 19
<212> RNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<400> 223
gaugacuuug guaucaaac   19

<210> 224
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      double stranded nucleic acid

<400> 224
guuugauacc aaagucauc   19